

OM of: US-09-623-304A-1 to: EST:\* out\_format : pfs

Date: Aug 21, 2002 9:40 PM

About: Results were produced by the GenCore software, version 4.5,  
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#### Command line parameters:

-MODEL=frame.p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US09623304/runat\_19082002.155554\_23745/app\_query.fasta.1.447  
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -VGAPOP=10.000 -VGAPEXT=0.500 -DELOP=6.000  
-DELETE=7.000 -START=1 -MATRIX=blom62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODEL=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500  
-MINLEN=0 -MAXLEN=200000000 -USER=US09623304 -CGN1.1.2744  
-NCPU=6 -ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30  
-NO\_XLPHY -WAIT -THREADS=1

#### Search information block:

Query: US-09-623-304A-1

Database: EST\*

Database sequences: 13736207

Search length: 184457050

Search time (sec): 1594.010000

#### score list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
gb_est2.BI143740	+ 1272.00	2595.41	2.6e-135	858	BI143740 602907395F1 NCI CGAP_K
gb_est2.BI144257	+ 1118.00	2279.06	1.1e-117	781	BI144257 602907822F1 NCI CGAP_K
gb_est2.BI143982	+ 979.00	1992.93	4.2e-102	753	BI143982 602908077F1 NCI CGAP_K
gb_est2.BI101237	+ 972.50	1981.11	9.2e-101	662	BI101237 602886939F1 NCI CGAP_K
gb_est2.BI101492	+ 934.00	1901.41	1.3e-96	686	BI101492 602886784F1 NCI CGAP_K
gb_est2.BF780854	+ 916.50	1864.80	1.3e-94	710	BF780854 602105743F1 NCI CGAP_K
gb_est2.BF789666	+ 896.50	1822.37	2.9e-92	783	BF789666 602105281F1 NCI CGAP_K
gb_est2.BF411612	+ 830.00	1690.36	6.6e-85	516	BF411612 U1-R-B1-bmp-d-10-0-U1
gb_est1.BB625105	+ 810.00	1646.16	1.9e-82	658	BB625105 BB625105 RIKEN full-1e
gb_hlc:AW011299	+ 807.00	1623.85	3.3e-81	2462	AK011299 Mus musculus 6 days n
gb_est2.BF789809	+ 792.50	1609.95	2.0e-80	665	BF789809 602105362F1 NCI CGAP_K
gb_est1.BB643863	+ 760.00	1543.39	1.0e-76	641	BB643863 BB643863 RIKEN full-1e
gb_est1.AM475637	+ 752.50	1526.49	8.8e-76	721	AM475637 un69d02.y1 Sugano mus
gb_est1.BB644922	+ 744.00	1510.22	7.1e-75	651	BB644922 BB644922 RIKEN full-1e
gb_est2.BI101289	+ 729.00	1478.18	4.1e-73	690	BI101289 602887019F1 NCI CGAP_K
gb_gss:CMS03W7	+ 690.50	1398.14	1.2e-68	753	AL263380 Tetraodon nigroviridis
gb_est1.AV603377	+ 674.50	1368.45	5.6e-67	575	AV603377 AV603377 Bos taurus ki
gb_est1.AV602053	+ 671.50	1359.18	1.8e-66	740	AV602053 AV602053 Bos taurus ki
gb_est1.AM226791	+ 656.00	1331.23	6.6e-65	533	AM226791 un62c03.y1 Sugano mus
gb_est1.AM318913	+ 644.00	1305.07	1.9e-63	559	AM318913 un09d03.y1 Sugano mus
gb_est1.AM107090	+ 641.50	1300.29	3.5e-63	581	AM107090 u192g12.y1 Sugano mus
gb_est1.AI747352	+ 635.00	1297.69	4.9e-63	398	AI747352 u105d05.y1 Sugano mus
gb_est1.AI227094	+ 625.00	1267.51	2.4e-61	525	AI227094 u119g11.y1 Sugano mus
gb_est2.BI550775	+ 622.50	1257.61	8.4e-61	774	BI550775 603195699F1 NIH.MGC.95
gb_est1.AL667662	+ 612.50	1234.68	1.6e-59	935	AL667662 AL667662 directional
gb_est1.BB622505	+ 608.00	1230.02	2.9e-59	641	BB622505 BB622505 RIKEN full-1e
gb_gss:CMS03U08	+ 608.00	1224.22	6.1e-59	1030	AL261452 Tetraodon nigroviridis
gb_est2.BF780894	+ 596.00	1217.64	1.4e-58	899	BF780894 602105040F1 NCI CGAP_K
gb_hlc:AK015481	+ 595.00	1197.50	1.3e-57	1212	AK015481 Mus musculus adult ma
gb_hlc:AK015907	+ 589.00	1192.37	3.6e-57	1557	AK015907 Mus musculus adult ma
gb_gss:AO223870	+ 589.00	1175.72	2.6e-57	461	AO223870 HS_2014_A2_H08_MR_C1T
gb_est1.AA989815	+ 580.00	1174.87	3.1e-56	484	AA989815 uc79d07.y1 Sugano mus
gb_est1.AA293349	+ 549.00	1111.59	1.1e-52	493	AA293349 un92d02.y1 Sugano mus
gb_est1.AM259025	+ 544.00	1102.61	3.6e-52	442	AM259025 un76e01.y1 Sugano mus
gb_est2.BG394461	+ 528.50	1063.17	5.7e-50	816	BG394461 602456588F1 NIH.MGC.16
gb_est1.AI788269	+ 521.50	1051.61	2.5e-49	645	AI788269 uk66a04.y1 Sugano mus
gb_est1.ALS583547	+ 517.50	1037.77	1.5e-48	1019	ALS583547 A2583547 LTI_FL015.B1
gb_est1.AM012077	+ 511.50	1033.48	2.6e-48	526	AM012077 un07e03.y1 Sugano mus
gb_est1.ALS528489	+ 502.50	1006.79	7.8e-47	1024	ALS528489 A1528489 LTI_NFL003_N
gb_est2.BI546348	+ 502.00	1006.04	8.6e-47	1001	BI546348 603188840F1 NIH.MGC_9

gb\_est2.BG972732 + 492.50 988.04 8.7e-46 879 | BG972732 602837519F1 NCI CGA  
gb\_est2.BG253799 + 491.50 984.95 1.3e-45 956 | BG253799 602366683F1 NIH.MGC  
gb\_gss:CMS020YX + 490.50 982.65 1.7e-45 975 | AI193074 Tetraodon nigroviridis  
gb\_gss:AQ471589 + 490.00 987.67 9.1e-46 594 | AQ471589 CITB1-EL-258818.TR  
gb\_est1.BE237514 + 489.50 988.24 8.5e-46 521 | BE237514 146834 MARC 4BOV BO

seq\_name: gb\_est2:BI143740

seq\_documentation\_block:

LOCUS BI143740 858 bp mRNA linear EST 05-JUL-2001

DEFINITION 602907395F1 NCI CGAP\_K1d14 Mus musculus CDNA IMAGE:5064407

5', mRNA sequence.

ACCESSION BI143740

VERSION BI143740.1 GI:14603741

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgi.nci.nih.gov/

AUTHORS 1 (bases 1 to 858)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Place: LAM1173 row: n column: 24

High quality sequence stop: 854.

Location/Qualifiers

1..858

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5064407"

/clone\_11b="NCI CGAP\_K1d14"

/lab\_host="PH10B (v1 phage-resistant)"

/note="Organ: kidney; Vector: pCMV-Sport6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.75 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library. |"

BASE COUNT 227 a 220 c 210 t

ORIGIN

alignment\_scores:

Quality: 1272.00 Length: 286

Ratio: 4.659 Gaps: 6

Percent Similarity: 95.455 Percent Identity: 90.210

alignment\_block:

US-09-623-304A-1 x BI143740 ..

Align seg 1/1 to: BI143740 from: 1 to: 858

87 IIleheglyserValIphetrPleuIIeAlaphetshISglaspLeuLe 103

|||||.....|

3 ATATTGGTTCANATTGGCTCATAGCCCTTTCATACGAGACCTATT 52

103 u.AsnasppProaspIleThrProCysValaspasValIhsserPheThr 119

|||||.....|

53 AACGCGATCCAGATATCACCCCTGTGTGACACACGTCATTCATTACG 102

120 GAlalaphelpeupheserleuGlulThrlInThrlleGlytyrGlyty 136

|||||.....|

103 GCTGCAATTTTATTCCTCGAGACCCAGACCACTTGAGTACGGGTTA 152

136 rArgCyValThrGlulGlysserValAlaValIleuMetValIleuG 153

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|||||
153 CCGCTGTGCACCGAAGAGTCTGTGTGCTGACTGACAGTGCCTTC 202
154 InsrIleuSerCysIleIleAsnThrPheIleIleGlyAlaIleu 169
155 |||||||
203 ACTCCATCTCCAGTGCATCATTAACACCTTCATCTGTGAGAGGCTTG 252
170 AlaIysMetAlaThrAlaArgLysArgAlaGlnThrIleArgPheSerTy 186
253 GGAAAGATGGCAACTGCCCGGAAGAGGCCAGACCATACGCTTCAGCTA 302
186 rPheAlaIleuIleGlyMetArgAspGlyLysIleuCysIleuMetTparG 203
303 TTTTCCCCCATTTGGTATGAGAGACGGGAAGCTTTCCTCATAGTGGCGCA 352
209 IeGIAspPheArgProAsnHisValIleGluGlyThrValArgAlaGln 219
353 TAGGTGACTTCGACCCAAACCATGTGTGAGAGGCGAGGTGAGAGGCCAA 402
220 LeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMetAlaPheLy 236
403 CTTTGCGCGTATTTCAGAACACAGTGAAGGAGAGATGACATGGCGTTAA 452
236 sAspLeuLysIleuValAsnAspGlnIleIleuValThrProValThrT 253
453 AGACCTCAAAACTGTCATGACAGACAGATTAATCCTGTACTCCAGTGACTA 502
253 IeValHisGluIleAspHisGluSerProLeuTyrAlaIleuAspArgLys 269
503 TTGTGTCATGACATTCGACCATGAGAGCCCTGTGTATCCCTTGACCGCAG 552
270 AlaValAlaLysAspAsnPheGluIleuValThrPheIleTyrThrG 286
553 GCAGTGGCCAAAGATTAATTCAGAGATTGTGTGACATTTATTATTAATCG 602
286 yAspSerThrGlyThrSerHisGlnSerArgSerTyrValProArg* 303
603 TGAATTCACATGGGACATCCACAGTCCAGAAATTCCTACATCCCGCAGAG 652
303 **IleLeuTyrPGLYHisArgPheAsnAspValIleuGluValLysArgLys 319
653 AAATTCCTCTGGGGCCACAGGCTTTCATGATGTATCGGAAGTGCACAGAGAA 702
320 ..TyrTyrLysValAsnCysLeuGln.PheGluGlySerValGluValTy 335
703 CGTACTACAAAGGTGAACCTGCTTGAAGTTGAAGAGCGTGAAGTCTA 752
335 rAlaA.ProPheCysSerAla.LysGlnLeuAspTyrLysAspGlnIle 351
753 CCGCCCCCTTTTGGAGTGCACAAACAGTGAAGAGGACCAACAAAT 802
351 uHis..IleGluLysAlaProProValArgLysCysThrSerasp 366
803 CAACAACGTGAGAACACACGCTCCCTGCCAGAGATCTCGCAATTCGAA 850

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seq\_name: gb\_est2:B1144257

seq\_documentation\_block:

LOCUS B1144257 781 bp mRNA linear EST 05-JUL-2001  
 DEFINITION 60290782JF1 NCL\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5064724  
 5' mRNA sequence.

ACCESSION B1144257

VERSION B1144257.1 GI:14604258

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eulhemia; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 781)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/MLN at:  
<http://image.llnl.gov>  
 Plate: L14M1174 row: 1 column: 05  
 High quality sequence start: 25  
 High quality sequence stop: 757.  
 Location/Qualifiers

#### FEATURES

1..781

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5064724"

/clone\_lib="NCL\_CGAP\_Kid14"

/lab\_host="DH10B (T1 phage-resistant)"

/note="Organ: kidney; Vector: pCMV-Sport6; Site: 1; NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.75 kb. Constructed by Life  
 Technologies. Note: this is a NCL\_CGAP Library. 1"

BASE COUNT

204 a 184 c 188 g 205 t

ORIGIN

#### alignment\_scores:

Quality: 1118.00 Length: 231

Ratio: 4.991 Gaps: 2

Percent Similarity: 96.970 Percent Identity: 91.775

#### alignment\_block:

US-09-623-304A-1 x B1144257 ..

Align seg 1/1 to: B1144257 from: 1 to: 781

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1 MetSerTyrTyrGlySerSerTyrHisIleAsnAlaAspAlaLysTy 17
89 ATGAGCTATTACGAGAGTAGTACGATGCTCAATGTCAGTCCAAATA 138
17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArg 34
139 TCCAGGCTATCCCTCCAGACATGCCATCGCTGAGAGAGAGCAAGAA 188
34 rArgPheLeuHisLysAspGlySerCysAsnValLyrPheLysHis 50
189 GGGCTTGTCCACAAAGATGGCAGCTGTATGTGACTTTTAAACAT 238
51 PheGlyLysTyrPGLYSerTyrValAlaAspIlePheThrThrLeuVal 67
239 TTTGGAGATGGGGAGCTACATGTTGATATTTTACACCTCTGTGGA 288
67 pThrLysTyrPArgHisMetPheValIlePheSerLeuSerTyrIleLeu 84
289 TACCAAGTGGCGCATATGTCTCAATATTTCTCTGTCTTACATTCCT 338
84 eTyrPheLeuIlePheGlySerValPheTyrPheLeuIleAlaPheHisGly 100
339 CCGGTGATATTGTTGCTTCATTTTGGCTCATACCTTTATCATCAGA 388
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
389 GACCTATTAAAGCATCCAGATATCACCCCTTGTGTGACAAAGTGCAT 438
117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGly 134
439 ATTATACGCTGCATTTTATCTCCCTGAGAGACCCAGACCATTTGAT 488
134 yGlyLysTyrArgCysValThrGluGluCysSerValAlaValLeuMet 150
489 ACGGTTACCGCTGTGTACCCGAAAGAGTGTCTGTGTGCTGTACTGAC 538

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151 11leuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAla 167
|||||
539 ATCCTTAGCCATCCCTCAGCTGATCATTAACACCTTCATCATTTGAGAC 588
167 aa1aleuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgp 184
|||||
589 AGCCTTGCAAGATGCGCACTGCCGGAAGAGCCAGACCATACGCT 638
184 hseSerTyrrPheAlaLeuIleGlyMetArgspGlyLysLeuCys.LeuMe 200
|||||
639 TCAGCTATTGTCCTCATTTGGTAGAGACGGGAAGCTTTGGCTTCAT 688
200 tTrrPArgIleGlyAspPheArgProAsnHisValIleGlyThrVala 217
|||||
689 GTGGCGATAGTGACTTCCGACAAACCATGTGGTAGAGGCGACGGTGA 738
217 rga1aGlnLeuLeuArgTyrrThrGluAspSerGluGlyArg 230
|||||
739 GAGCCCAACTTCGCGCTAT.....CAGAAGAAAGAGAG 773

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seq\_name: gb\_est2:B1143982

seq\_documentation\_block:

LOCUS B1143982 753 bp mRNA linear EST 05-JUL-2001  
 DEFINITION 602908077F1 NCI CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5065051  
 5', mRNA sequence.

ACCESSION B1143982  
 VERSION B1143982.1 GI:14603983

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: c9apbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM1175 row: 1 column: 20

High quality sequence stop: 725.

Location/Qualifiers

1. 753

/organism="Mus musculus"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5065051"

/clone.lib="NCI CGAP Kid14"

/lab.host="DH10B (TI phage-resistant)"

/note="Organ: Kidney; Vector: pCMV-Sport6; Site.1: NotI; Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library. I"

BASE COUNT 212 a 166 c 171 g 204 t

ORIGIN

alignment\_scores:

Quality: 979.00 Length: 210

Ratio: 4.847 Gaps: 2

Percent Similarity: 96.190 Percent Identity: 89.524

alignment\_block:

US-09-623-304a-1 x B1143982 ..

Align seg 1/1 to: B1143982 from: 1 to: 753

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1 MetSerTyrrGlySerSerTyrrHisIleIleAsnAlaAspAlaLysTy 17
|||||
127 ATGAGCTATTAGGAGATGCTACAGATGTGTCAATGTGCACTCCAAATA 176
17 rProGlyTyrrProProGluHisIleIleAlaGluLysArgArgAlaArg 34
|||||
177 TCAGAGCATCTCCAGAGCATGCGCATGCTGAGAGAGAAAGAGCAAGAA 226
34 rga1aGlnLeuHisLysAspGlySerCysAsnValTyrrPheLysHisIle 50
|||||
227 GGCCTTGCTCCACAAAGATGCGAGCTGTAATGCTATCTTAAACACATT 276
51 PheGlyGluTrrPglySerTyrrValValAspIlePheThrThrIleVal 67
|||||
277 TTGTGAGAAATGGGAGCTACATGTTGATATTTTATACACCTCTTGGA 326
67 rThrLysTrrPArgHisMetPheValIlePheSerLeuSerTyrrIleLeu 84
|||||
327 TACCAAGTGGGCGCATATGTTCAATATTTCTCTGCTTACATTCCT 376
84 eTrrPleuIlePheGlySerValPheTrrPleuIleAlaPheHisGly 100
|||||
377 CCTGTTGATATTGTTGCTCATATTGCTCATAGCCTTCATCACGGA 426
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
|||||
427 GACCTATTAGAGATCCAGATATCACCCCTGTGTGTAACAGTGCATTC 476
117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGly 134
|||||
477 ATTACAGGCTCATTTTATTTCTCCCTGAGACACCAAGCAGCATTTGAT 526
134 YrGlyTyrrArgCysValThrGluGlyCysSerValAlaValLeuMetVal 150
|||||
527 ACGGTTACCGCTGTGTCCACGAAAGTCTGTGCGCTACTACAGTG 576
151 11leuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAla 167
|||||
577 ATCCTTAGTCATCCTCAGCTGATCATTAACACCTTCATCATTTGAGAC 626
167 aa1aleuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleAr 183
|||||
627 AGCCTTGCAAGATGCGCACTGCCGGAAGAGAGCAGACCATACG 676
183 gPheSerTyrrPheAlaLeuIleGlyMetArgspGlyLysLeuLeu 200
|||||
677 GTTCAGGATATTGGCCCTCTATGATGAGAGAGCGGAAGTT.TGCCATCA 725
200 eTrrPArgIleGlyAspPheArgPro 208
|||||
726 TGTGGGAAATAGTGAATTCGACCA 751

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seq\_name: gb\_est2:B1101237

seq\_documentation\_block:

LOCUS B1101237 662 bp mRNA linear EST 26-JUN-2001  
 DEFINITION 602886939F1 NCI CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5042480  
 5', mRNA sequence.

ACCESSION B1101237

VERSION B1101237.1 GI:14552130

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: c9apbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

Plate: LLM1116 row: m column: 09  
High quality sequence start: 24  
High quality sequence stop: 660.  
Location/Qualifiers

## FEATURES

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1..662  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5042480"  
/clone\_lib="NCI CGAP Kid14"  
/lab\_host="DH10B (TI phage-resistant)"  
/note="Organ: kidney; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library. |"  
BASE COUNT 160 a 168 c 152 g 182 t  
ORIGIN

alignment\_scores:  
Quality: 972.50 Length: 216  
Ratio: 4.698 Gaps: 5  
Percent Similarity: 95.833 Percent Identity: 89.815

alignment\_block:

US-09-623-304A-1 x B1101237 ..

Align seg 1/1 to: B1101237 from: 1 to: 662

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52 GlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAspH 68
|||||
23 GGAGAAATGGGGGAGTACATGTTGATATTATTTACACCTGTGTGATAC 72
|||||
68 rTyrTrpATGHisMetPheValIlePheSerLeuSerTyrIleLeuSer 85
|||||
73 CAAGTGGCCCATATGTCATATATTTCTGCTTACATCTCTCC 122
|||||
85 rPleuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGlyasp 101
|||||
123 GGTGTGATATTGTTCATATTTGGCTCATAGCTTTCATCAGGAGAC 172
|||||
102 LeuLeuAsnAspProAspIleThrProGlyValAspAsnValHisSerP 118
|||||
173 CTATTAGCGATCCAGATATACCCCTGTGTGACACGTCATTCATT 222
|||||
118 eThrGlyAlaPheLeuPheSerLeuGluThrGlnThrIleGlyTyrG 135
|||||
223 TACGGCTGCAATTTTATTCCTCGAGACCCAGACCATTCGATGAC 272
|||||
135 lYTYrArgGlyValThrGluGlyCysSerValAlaValLeuMetValIle 151
|||||
273 GTTACCGCTGTGCACGAGAGTCTCTGTGCTACTGACAGAGTGCATC 322
|||||
152 LeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAla 168
|||||
323 CTTCAGTCCATCTCAGCTGCATCATTAACACCTTCATCTTGAGACAGC 372
|||||
168 AlaValAla.LysMetAlaThrAlaArgLysArgLagIleThrIleAcpHe 184
|||||
373 CTTCGGCCAAAGATGCACTGCCCGGAGAGAGCCAGACCATACGCTTC 422
|||||
185 SerTyrPheAlaLeuIleGlyMetArg.AspGlyLys.LeuCysLeuMet 200
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423 ACCATTATTTGGCCCTCATGTGTATGAGACGAGGAGCGCTTGCCTCATG 472
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201 TTPATGIIleGlyAspPheArgProAsnHisValValGluGly...Thra 216
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473 TGGCGCATGATGACTTCCGACCAACCATGTGTCAGAGGCGCGTGC 522
216 lArgAlaGlnLeuLeuArGTrpThrGluAspSerGluGlyArgMetThrm 233
|||||
523 AGAGCCACACTTCTGGCTATTCAAGACACTGACGGAGGATGACGA 572
233 eAlaIaPhe.LysAspLeuLysLeuValAsnAspGlnIleIleLeuValTh 249
|||||
573 TGGCGTTTACAGACCTCAAACTGTCATATGACAGATATCTGTGTAAC 622
249 rProValThrIleValHisGluIleAspHisGluSerPro 262
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DEFINITION 602887284F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:5042372  
5', mRNA sequence.  
ACCESSION B1101492  
VERSION B1101492.1 GI:14552385  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Tissue Procurement: Jeffrey E. Green, M.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Contact: Robert Strausberg, Ph.D.  
Unpublished (1999)  
National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT

CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LLM1116 row: h column: 21  
High quality sequence stop: 684.  
Location/Qualifiers

## FEATURES

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Average insert size 1.75 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library. |"  
BASE COUNT 194 a 155 c 150 g 187 t  
ORIGIN

alignment\_scores:  
Quality: 934.00 Length: 188  
Ratio: 5.049 Gaps: 0  
Percent Similarity: 98.404 Percent Identity: 92.021

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Align seg 1/1 to: B1101492 from: 1 to: 686

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1 MetSerTyrTyrGlySerTyrHisIleIleAsnAlaAspAlaTyr 17
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109 ATGAGCTATTACGAGATGACGATGTCATATGTGATCGCAATAA 158
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17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArg 34
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|||||
159 TCAGGCTATCTCCAGAGCATGCGTGGAGAGAGAGACAGAA 208
34 rgtatgLeuLeuHisLysAspGlySerCysAsnValTyrPheHisIle 50
|||||
209 GGGCTTGATGCCAAGATGGCAGCGTATGTACTTTAAACACATT 258
51 PheGlyIuTyrPglSerTyrValValAspIlePheThrPheLeuValAs 67
|||||
259 TTGGAGAAATGGGGAGCTACATGTTGATATTTTACCATCTTGTGGA 308
67 pThrLysTyrPArgHisMetPheValIlePheSerLeuSerTyrIleLeu 84
|||||
309 TACCAAGTGGCCCATGTTCATTAATATTTTCTGCTTACATTCCTCT 358
84 erTrrPleuIlePheGlySerValPheTrrPleuIleAlaPheHisGly 100
|||||
359 CCGTGTGATATTGGTTCATATTAGGCTCATAGCCCTTTCATCACGGA 408
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
|||||
409 GACCTATTAAAGCATCCAGATATCACCCCTGTGTTCACAACGTGCATT 458
117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGly 134
|||||
459 ATTACGGCTGATTTTATTTCCTCGAGACCCAGACACCATTTGGAT 508
134 TyrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMet 150
|||||
509 ACGGTACCCCTGTGTACCGAAGAGCTGTGTGTGTACGTACACAGTG 558
151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGly 167
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559 ATCTTCAGTCCATCTCAGCTGATCATATAACCTTCATTCATTGGAG 608
167 aAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArg 184
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609 AGGCTTGGCAAGATGGCACTGCCGGAAGAGAGCCACCATATAGCT 658
184 hSerTyrPheAla 188
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659 TCAGCTATATTGCC 672

seq_name: gb_est2:BF780854

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DEFINITION 602105743F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4223626
5', mRNA sequence.
ACCESSION BF780854
VERSION BF780854.1 GI:12085887
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NID-MGC http://nidl.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgsb@r-mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLM9812 row: f column: 11
High quality sequence stop: 703.
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/organism="Mus musculus"
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/clone_11b="NCI_CGAP_Kid14"
/lab_host="DH10B (71 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-Sport6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. !"

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ORIGIN

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Quality: 916.50 Length: 190
Ratio: 4.927 Gaps: 1
Percent Similarity: 97.895 Percent Identity: 92.105

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2 GAGCGAAGCTTTCCTCATGTGCGCATAGTGACTCCGACCAACCA 51
210 sValValGluGlyThrValArgAlaGlnLeuLeuArgTyrThrGluAsp 227
|||||
52 TGTGTAGAGGCGCAGCGGTGAGAGCCCAACTTCTCGCTATTCAGAGA 101
227 erGluGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsp 243
|||||
102 GTGAAGGAGAGATGACGATGCGCTTAAAGCCCAACTGTCATTAAGAC 151
244 GlnIleIleLeuValThrProValThrIleValHisGlnIleAspHis 260
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152 CAGTAATTCCTGTAACCTCAAGTACTATTGTCCATATAATTGACATGA 201
260 uSerProLeuTyrAlaLeuAspArgLysAlaValAlaLysAspAsnPhg 277
|||||
202 GAGCCCTCTGTATGCCCTTGACCGCAAGCGAGTGGCCAAAGATATTGCG 251
277 IuIleLeuValThrPheIleTyrThrGlyAspSerThrGlyThrSerHis 293
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252 AGATTCTGTGTGACATTATTATTACTGTGTGATTCACCTGGACATCCAC 301
294 GlnSerArgSerSerTyrValProArg**IleLeuTrrPglYrHisArgPh 310
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302 CAGTCCAGAAAGTTCTTACATCCCCAGAGAAATTTCTTGGGGCCACAGTT 351
310 eAsnAspValLeuGluValLysArgLysTyrTyrLysValAsnCysLeuG 327
|||||
352 TCATGATGATTTGGAAAGTGAAGAAAGTACTCAAGGTGAACTGCTTGC 401
327 IuPheGluGlySerValGluValTyrAlaProPheCysSerAlaLysGln 343
|||||
402 AGTTTGAAGAGAGCGTGAAGTCTACGCCCTTTTTCACATGCGCAACAA 451
344 LeuAspTrrPylsAspGlnGlnLeu...HisIleGluLysAlaProProVa 359
|||||
452 CTGGACATGGAGAGCAACCAACTCAACACTTGGAGAAAAGTCCCTTGC 501
359 IArgGluSerCysThrSerAspThrLysAlaArgArgSerPheSerA 376
|||||
502 CCGAGATCTCTGCAATTCGACACCAACACAGAGAGCGGTCTCTTACGC 551
376 IAlaValAlaIleValSerSer 382
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552 CAGTTCGTGTGTGAGCAGC 571

seq_name: gb_est2:BF789666

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  ACCESSION  BF789666
  VERSION    BF789666.1 GI:12094702
  KEYWORDS   EST.
  SOURCE      house mouse.
  ORGANISM   Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE  1 (bases 1 to 783)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              Tissue Procurement: Jeffrey E. Green, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNU at:
              http://image.llnl.gov
              Plate: LHM9811 row: b column: 22
              High quality sequence stop: 721.
              Location/Qualifiers
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                  /strain="FVB/N"
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                  /lab_host="DH10B (T1 phage-resistant)"
                  /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.75 kb. Constructed by Life
                  Technologies. Note: this is a NCI CGAP library. 1"
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|||||
147 ATGACGCTATTACGGAAGTAGTACAGAGATTGTCAATGTCGACTCCAAATA 196
17 rProGlyTyrProProGluHisIleIleIleAgluIuysArGArGAlaArG 34
|||||
197 TCCAGGCTATCTCTCCAGAGCATGCGCTGAGAGAGAGACAGCAAGAA 246
34 rGArLeuLeuHisIysAspGlySerCysAsnValTyrPheIysHisIle 50
|||||
247 GCGCGTTCGTCACAAAGATGCGACCTGAATGTACTTTAAACACATT 296
51 PheGlyGluTrpGlySerTyrValValAspIlePheIleThLeuValAs 67
|||||
297 TTTGGAGATGGGGAGGACTACATGGTGAATATTTTACCACTCTGTGGA 346
67 pThrIysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84
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347 TACCAAGTGGCGCCATATGTCATATAATTTTCTCTGTCTTACATTTCT 396

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84 exTrPleuIlePheGlySerValPheTrPleuIleAlaPheHisHisGly 100
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397 CCGGTGTGATATTTGGTCCATATTTGGCTCATACCTTTTCATCACGA 446
101 AspPleuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
|||||
447 GACCTATTAGGCAATCCAGATATACACCCCTTGTGTGAACGTCATTC 496
117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnTrpThrIleGlyT 134
|||||
497 ATTTACGCGCTGCATTTTATTCCTCCGTGAGACCCGACGACCATTTG 546
134 yreGlyTyrArgCysValThr.GluGluCysSerValAlaValLeuMet 150
|||||
547 ACGGTACCGCGCTGTGCACCCGCAAGAGTCTCTGTGGCTGTACTGAC 596
150 IileGluGlnSerIle.LeuSerCysIleIle.AsnThrPheIleIleG 166
|||||
597 GATCCTTCAGTCATCCCTCAGCTGCATCATTAACACCTTCATCATTC 646
166 yAlaAla.LeuAlaIysMetAlaThrAlaArgLys.ArgAlaGlnThr 182
|||||
647 AGCAGCCTTTGGCAAGATGGGACACTGCCGGAAGAGAGAACGACAA 696
182 leArgPheSerTyrPheAlaLeuIleGlyMet...ArgAspGlyLysLeu 197
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697 TAACTTCAGATTATTTGGCCCTCATTTGGTTGAAAGCGGGAACCTT 746
198 CysLeuMetTrp 201
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747 TGCCTCATGTGG 758
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  DEFINITION  UT-R-BT1-bmp-d-10-0-UT-s1 UT-R-BT1 Rattus norvegicus cDNA clone
  ACCESSION  BF411612
  VERSION    BF411612.1 GI:11399601
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  SOURCE      Norway rat.
  ORGANISM   Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
  REFERENCE  1 (bases 1 to 516)
  AUTHORS    Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE      Normalization and subtraction: two approaches to facilitate gene
              discovery
  JOURNAL    Genome Res. 6 (9), 791-806 (1996)
  MEDLINE    97044477
  COMMENT    Contact: Soares, MB
              Program for Rat Gene Discovery and Mapping
              University of Iowa
              451 Eckstein Medical Research Building Iowa City, IA 52242, USA
              Tel: 319 335 8250
              Fax: 319 335 9565
              Email: mosares@blue.weeg.uiowa.edu
              The sequence contained an oligo-dT track that was present in the
              oligonucleotide that was used to prime the synthesis of first
              strand cDNA and therefore this may represent a bonafide poly A
              tail. The sequence tag present in the cDNA between the NotI site
              and the oligo-dT track served to identify it as a clone from the
              normalized mid-brain library cDNA library preparation: M.B. Soares
              Lab Clone distribution: clones will be available through Research
              Genetics (www.resgen.com)
              Seq primer: M13 Forward
              POLYA=Yes.
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                    /strain="Sprague-Dawley"

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/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The library
UI-R-B71 is a subtracted library derived from a mixture of
the following tissues: hippocampus, thalamus, mid-brain,
medulla, corpus striatum, cerebral cortex and testis. For
a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-B71
TAG_TISSUE=mid-brain
TAG_SEQ=GATCG"

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    Ratio:        5.061      Gaps:      0
Percent Similarity: 97.619      Percent Identity: 94.643

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US-09-623-304a-1 x BF411612/rev ..

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516 CATATGTTTGAATATTTCTTCTTCTTCAACATCTCTCTCTGTTGATGATTT 467
88 eglSerValPheTrpleuIIealIaphehIshIsgIYaspleuIeasna 105
466 CGGCCCATATTTTGCTCATAGCCCTTCATCAGAGAGACCTATTAAAGCG 417
105 sPrOasPleIeThProCysValasPasnValHisSerPheThrGlyAla 121
416 ATCCAGACATCACCCCGTGGCGACAAACGATTCATTATACGGCGCG 367
122 PheIeupheserleuGluThrGlnThrThrlleGlyrrGlyTyrrAGcy 138
366 TTTTATCTCTCCCTTGAGACCCCAACACCAATCGGGTACGGTTACCGTGG 317
138 sValThrGluGluCysSerValAlaValIleuMetValIleuGlnSeri 155
316 TGTACGGAAGAAATGCTGTGTGGCGGTGCATCGGTCACTCTTCAGTCCA 267
155 leIeuserCysIleIleasnThrPheIleIleGlyIaAlaIeuaAlaYs 171
266 TCCGAGACTGCATCAATAACACCTTCATTCATGGGGCAGCCTTGCAAG 217
172 MetaIthAlaArgLysArgAlaGlnThrlleArghPheSerTyrrPheAl 188
216 ATGGCGACCCCGCGAAGCGAGCCAGACATCGGCTTCAGCTATTTTCGC 167
188 aleuIIeGlyMetArgaspGlyLysleuCysIleuMetTrrPrgIIeGlyA 205
166 ACTCATCGGCATGAGACGCGGAAGCTTGGCTCATGATGGCGCATAGGTG 117
205 sPrPheArghProAsnHisValAlaGluGlyThrValArgAlaGlnIleu 221
116 ACTTCCAGACCAACCATGTGGTGGAGGCGACGAGAGCCCAACTTCTG 67
222 ArgThrThrGluAspSerGluGlyArgMetThrMetAlaPheLysAspLe 238
66 CGCATTCACAGACAGACGGAAGGGCGGATGCATGCGCTTAAAGACCA 17
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111
16 AAAA 13
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seq_documentation_block:
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DEFINITION BB625105 RIKEN full-length enriched, adult male cecum Mus musculus
ACCESSION  BB625105
VERSION     BB625105.1 GI:16463440
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 658)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y., and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,T., Aizawa
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
FEATURES
source
Location/Qualifiers
1..658
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/dev_stage="adult"
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/Note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia

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	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
	AK017299	2462 bp mRNA linear clone; Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:543041IM10.potassium inwardly-rectifying channel, subfamily J, member 12, full insert sequence.	AK017299.1	GI:12856469	HTC: CAP trapper.	Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.	Carninci,L.P., and Hayashizaki,Y.	

JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253

**TITLE**  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs for  
prepare full-length cDNA libraries for rapid discovery of new genes

REFERENCE	3 (sites)
AUTHORS	
Shibata, K.,	
Itoh, M.,	
Aizawa, K.,	
Nagaoka, S.,	
Sasaki, N.,	
Carninci, P.,	

Sunni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Fujiwara, K.

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
Riken integrated sequence analysis (RISA) system---384-format  
sequencing pipeline with 384 multicapillary sequencer

MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4 (sites)

<b>TITLE</b>	<b>FANTOM Consortium.</b>
<b>JOURNAL</b>	<b>Functional annotation of a full-length mouse cDNA collection</b>
	<b>Nature 409, 685-690 (2001)</b>

**AUTHORS**  
Adechi, T., Aikawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arikawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,

Hume,D., Imotani,K., Ishii,Y., Itoh,H., Kasukawa,T.,  
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K.,

Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasakii, D., Schimml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

TITLE Yasunishi, A., Yoshida, K., Yoshino, M., and Hayashizaki, Y.  
Direct Submission

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

COMMENT  
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and genome Science Laboratory in RIKEN.



ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 665)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNL at:  
<http://image.llnl.gov>  
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 ORIGIN  
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 421 GACCTATTAAAGCATCCAGATATCACCCCTTGCT. GACACGTCGCAATC 469  
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 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 641)  
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,  
 Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,U., Kono,H., Kouda  
 ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,  
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki  
 ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,  
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,  
 Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 UNPUBLISHED (2001)  
 COMMENT Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center(GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: [genome-resgsc.riken.go.jp](mailto:genome-resgsc.riken.go.jp),  
[urrl:http://genome.gsc.riken.go.jp/](mailto:urrl:http://genome.gsc.riken.go.jp/)  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh  
 ,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Iwawa,M., Ohara,E.,  
 Watanaki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura  
 ,S., Kawai,U., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and  
 Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Kono,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara  
 ,Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa  
 ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,  
 Ishii,Y. and Hayashizaki,Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
 Func. Genomics 2 pre, 172-186 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.  
 e mouse tissues.  
 Location/Qualifiers

FEATURES





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 Ratio: 5.314 Gaps: 0  
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US-09-623-304a-1 x BB644922 ..

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 ACCESSION BI101289  
 VERSION BI101289.1 GI:14552182  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NIH-MGC http://mgc.nci.nih.gov/  
 1 (bases 1 to 690)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: LLAM1116 row: e column: 06

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 High quality sequence stop: 651.  
 Location/Qualifiers

## FEATURES

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 ORIGIN

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US-09-623-304a-1 x BI101289 ..

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  |||||.....|.....|.....|.....|.....|.....|.....|
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OM of: US-09-623-304A-1 to: GenEmbl.\* out\_format : pfs  
Date: Aug 21, 2002 10:12 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

-MODL=frame+P2n.model -DEV=xlh  
-O=/cgn2.1/USPIO.spool/US09623304/runat\_19082002\_155555\_23758/app\_query.fasta.1.447  
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-EGAPOP=6.000 -EGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTWMT=pfs  
-NORR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09623304.@CGN1.1.4250 -NCPU=6 -ICPU=3 -LONGLOG  
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Query length: 383  
Database: GenEmbl.\*  
Database sequences: 1797656  
Search length: 187333701  
Search time (sec): 1882.350000

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1 (bases 1 to 1257)  
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Bennett,P.B. and Swanson,R.  
The human inward rectifier K+ channel subunit Klr5.1 maps to  
chromosome 17q25 and is expressed in kidney and pancreas  
Unpublished  
2 (bases 1 to 1257)  
Li,Y. and McKenna,E.  
Submitted (20-AUG-1999) Bioinformatics, Merck & Co., Inc.,  
WP42-300, West Point, PA 19486, USA

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DEFINITION Sequence 42 from Patent WO0146258.
ACCESSION AX179754
VERSION AX179754.1 GI:15132118
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REFERENCE
1 (bases 1 to 1730)
AUTHORS Baughn,M.R., Burford,N., Au-Young,J., Lu,D.A., Yang,J., Reddy,R.,
Lal,P., Hillman,J.L., Azimzai,Y., Yee,H., Nguyen,D.B., Yao,M.G.,
Gandhi,A.R., Tang,Y.T. and Khan,F.A.
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JOURNAL Patent: WO 0146258-A 42 28-JUN-2001;
Incyte Genomics, Inc. (US)
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location/Qualifiers
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ACCESSION  AF153817
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SOURCE     human.
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REFERENCE  1 (bases 1 to 1856)
            Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
            Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
            Karschin,A.
            Genetic and functional linkage of Kir5.1 and Kir2.1 channel
            subunits
            FEBS Lett. 491 (3), 305-311 (2001)
JOURNAL    PUBMED 11240146
REFERENCE  2 (bases 1 to 1856)
            Derst,C.
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DEFINITION Homo sapiens clone 1 inwardly-rectifying potassium channel Kir5.1
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REFERENCE
1 (bases 1 to 2089)
Dersl.C., Karschin.C., Wischmeyer.E., Hirsch.J.R.,
Preisig-Muller.R., Rajan.S., Engel.H., Grzeschik.K., Daut.J. and
Karschin.A.
Genetic and functional linkage of Kir5.1 and Kir2.1 channel
subunits
JOURNAL FEBS Lett. 491 (3), 305-311 (2001)
PUBMED 11240146
REFERENCE
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gene, exon 5 and complete cds, alternatively spliced.
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VERSION AF153814.1 GI:8132310
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 3642)
Derst.C., Karschin,C., Mischmeyer,E., Hirsch,J.R.,
Preisig-Muller,R., Rajan,S., Engel,H., Grieschik,K., Daut,J. and
Karschin,A.
Genetic and functional linkage of Kir5.1 and Kir2.1 channel
subunits
JOURNAL FEBS Lett. 491 (3), 305-311 (2001)
PUBMED 11240146
REFERENCE
2 (bases 1 to 3642)
Derst.C.
Direct Submission
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Deutschhausstr. 2, Marburg 35037, Germany
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1 (bases 1 to 4021)
Derst,C., Karschin,C., Wischmeyer,E., Hirsch,J.R.,
Preisig-Muller,R., Rajan,S., Engel,H., Grzeschik,K., Daut,J. and
Karschin,A.
Genetic and functional linkage of Kir5.1 and Kir2.1 channel
subunits
JOURNAL FEBS Lett. 491 (3), 305-311 (2001)
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Derst,C.
AUTHORS

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TITLE Direct Submission  
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 1 (bases 1 to 123211)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 17, clone hRPK.1064\_E\_11  
 Unpublished  
 2 (bases 1 to 123211)  
 Birren,B., Fasmann,K., Linton,L., Nusbaum,C., Lander,E., Allen,N.,

**TITLE** Direct Submission  
**JOURNAL** Submitted (30-JUN-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
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**AUTHORS** Birren, B., Fasmann, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

**TITLE** Direct Submission  
**JOURNAL** Submitted (29-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

**TITLE** Direct Submission  
**JOURNAL** Submitted (31-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
**COMMENT** On Jul 31, 1998 this sequence version replaced gi.13347827. All repeats were identified using RepeatMasker: Smt, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Only the first 123.2 kilobases of this clone are being submitted. The remainder overlaps accession AC005242 (WTCR project L341).

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REFERENCE  1 (sites)
AUTHORS    Tracey A.
TITLE      Direct Submission
JOURNAL    Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
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            humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On Feb 1, 2002 this sequence version replaced gi:18476962.

COMMENT    ----- Genome Center
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            Web site: http://www.sanger.ac.uk
            Contact: humquerry@sanger.ac.uk
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            Center project name: BM408D5
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Rattus.  
REFERENCE 1 (bases 1 to 1260)  
AUTHORS Tucker,S.J., Imbrici,P., Salvatore,L., D'Adamo,M.C. and Pessia,M.  
TITLE pH dependence of the inwardly rectifying potassium channel, Kir5.1,  
and localization of the inwardly tubular epithelia  
JOURNAL J. Biol. Chem. 275 (22), 16404-16407 (2000)  
MEDLINE 20287495  
REFERENCE 2 (bases 1 to 1260)  
AUTHORS Tucker,S.J. and Pessia,M.  
TITLE Direct Submission  
JOURNAL Submitted (24-MAR-2000) University Laboratory of Physiology, Oxford

University, Parks Road, Oxford, Oxon OX1 3PT, United Kingdom  
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 AUTHORS Horio,Y.

TITLE Direct Submission  
 JOURNAL Submitted (11-JUL-1998) Yoshiyuki Horio, Faculty of Medicine, Osaka University, Department of Pharmacology II; 2-2 Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:horio@pharma2.med.osaka-u.ac.jp, Tel:81-6-879-3512, Fax:81-6-879-3519)  
 REFERENCE 2 (sites)  
 AUTHORS Mouri,T., Kitaka,N., Horio,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A. and Kurechi,Y.  
 TITLE Assignment of mouse inwardly rectifying potassium channel Kcnj16 to the distal region of mouse Chromosome 11  
 JOURNAL Genomics 54 (1), 181-182 (1998)  
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801 CCGCAAGGAGTGGCCAAAGATTAATTCGAGATTCTGTGACATTTATTT 850
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284 ythrghlyaspserrhrglythrserhisglinserargserertyval 300
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851 ATACTGTGATTCACCTGGACATCCACCACATCCAGAAAGTTCTCATATC 900
      |||
301 Proarg**lleuutrpglyhisargpheasnaspsvalleuvally 317
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901 CCGAGGAAATTCCTGGGGCCACAGTTTCATGATGATTTGGAAGTGAA 950
      |||
317 sarglystyrrlysvalasnrcysleuglnphegluglyservalgluv 334
      |||
951 GAGAAAGTACTACAAAGTGAAGTGTGCAAGTTTGAAGGAAAGCTGGAAG 1000
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334 altyrtrlapropheyserralalysgluleuasprrplysaspgingln 350
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1001 TCTACGCCCTTTTGCAGTGCACAAACACTGGAGCTGGAAGGACCAACAA 1050
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351 leu...hisileglulysalaprovalargglusercysrheseras 366
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1101 CACCAACACGAGGAGGCTCTTCAGCCAGTTCGCTGTGAGAGAGC 1149

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seq\_name: gb\_to:RNIRPC9

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seq_documentation_block:
LOCUS      RNIRPC9              1155 bp      mRNA      linear      ROD 11-JAN-1996
DEFINITION R.rattus mRNA for inward rectifier 9.
ACCESSION  X83581
VERSION    X83581.1 GI:609671
KEYWORDS   Inward rectifier potassium channel.
SOURCE     black rat.
ORGANISM   Rattus rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 1155)
AUTHORS   Bond,C.T., Pessia,M., Xia,X.M., Lagrutta,A., Kavanaugh,M.P. and
            Adelman,J.P.
TITLE      Cloning and expression of a family of inward rectifier potassium
            channels
JOURNAL    Recept. Channels 2 (3), 183-191 (1994)
MEDLINE    95179470
REMARK     Erratum: [[published erratum appears in Receptors Channels
            1994;2(4):following 350]]
REFERENCE  2 (bases 1 to 1155)
AUTHORS   Adelman,J.P.
TITLE      Direct Submission
JOURNAL    Submitted (19-DEC-1994) J.P. Adelman, Volium Institute for Advanced
            Biomedical, Research (VIABR), Oregon Health Sciences University,
            L474, 3181 SW Sam Jackson Park Rd., Portland OR 97201, USA

FEATURES
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             /db_xref="SWISS-PROT:P52191"
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            NPTIIGALIAAMATARKRAQTIRSFALICMRGKLCIMRIDFERNHYEGTVRA
            OLIRYSEDSERMTMAEFKDLKLVNDQIILVPTVIVIEIDHESPLVALDRKAVAKNF
            EILVFTYTGSTGSHOSRSSYVPRLEIWMHRRHYDEVKRYKVCVLCIQFEGSVEY
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            NPTIIGALIAAMATARKRAQTIRSFALICMRGKLCIMRIDFERNHYEGTVRA
            OLIRYSEDSERMTMAEFKDLKLVNDQIILVPTVIVIEIDHESPLVALDRKAVAKNF
            EILVFTYTGSTGSHOSRSSYVPRLEIWMHRRHYDEVKRYKVCVLCIQFEGSVEY
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BASE COUNT      294 a      295 c      291 g      275 t
ORIGIN
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    Quality: 1885.50      Length: 384
    Ratio: 5.001          Gaps: 2
    Percent Similarity: 98.177      Percent Identity: 93.229
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US-09-623-304A-1 x RNIRPC9
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1 ATGAGCTATATACGAGAGTAGCTACCGAATGTCAACAGTGCAGACTCCAAATA 50
|||||
17 rprogllytyrproprogluHisIleIleAlaGluLysArgAlaArgA 34
|||||
51 TCCAGGCTATCCCTCCAGAGATGCCATAGCCGAGAGAGAGACGACAGA 100
|||||
34 rgrtrleuHnHisLysAspGlySerCysAsnValLyrPheLysHisIle 50
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101 GGCGCTGTCTCCACAAAGATGGAGCTGTATGCTTGTAAACACATT 150

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seq_name: gb_htg:AC025586
seq_documentation_block:
LOCUS      AC025586                      187774 bp    DNA       linear   HTG 06-SEP-2000
DEFINITION Mus musculus clone RP23-320C8, WORKING DRAFT SEQUENCE, 7 unordered
            pieces.
ACCESSION  AC025586
VERSION    AC025586.3  GI:9972313
KEYWORDS   HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE     mouse mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 187774)
AUTHORS    McComb,M.R., Baker,J.P., Bahret,A., Bal,H., Dedhia,N.N., de la
            Bastille,M., Huang,E.N., King,L., Kirchoff,K.A., Miller,B.,
            Nascento,L.U., O'Shaughnessy,A.L., Preston,R.R., Rodriguez,M.A.,
            Shah,R.S., Shekher,M., Spiegel,L.A., Toth,K. and Vil,M.D.
            Mouse Genomic Sequence
            Unpublished
            2 (bases 1 to 187774)
            McComb,M.R.
            Direct Submission
            Submitted (13-MAR-2000) Lita Annenberg Hazen Genome Sequencing
            Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
            Harbor, NY 11724, USA
            On Sep 6, 2000 this sequence version replaced gi:8459867.
            ----- Genome Center
            Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
            Laboratory
            Center code: CSHL
            Web site: http://www.cshl.org/genseq
            Contact: mccomb@cshl.org
            ----- Project Information
            Center project name: RP23-320C8
            Center clone name: RP23-320C8
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 62545: contig of 62545 bp in length
            * 62546 62975: gap of unknown length
            * 62976 123025: contig of 60050 bp in length
            * 123026 123454: gap of unknown length
            * 123455 145175: contig of 21721 bp in length
            * 145176 145604: gap of unknown length
            * 145605 166987: contig of 21383 bp in length
            * 166988 167416: gap of unknown length
            * 167417 180022: contig of 12606 bp in length
            * 180023 180451: gap of unknown length
            * 180452 184785: contig of 4334 bp in length
            * 184786 185214: gap of unknown length
            * 185215 187774: contig of 2560 bp in length.
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BASE COUNT  55776 a 37551 c 37806 g 54065 t 2576 others

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 Ratio: 4.810 Gaps: 3  
 Percent Similarity: 96.364 Percent Identity: 91.169

alignment\_block:  
 US-09-623-304A-1 x AC025586/rev ..

Align seg 1/1 to reverse of: AC025586 from: 1 to: 187774

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17 rProGlyTyrProProGluHisIleIleAlaGluYusArgArgAlaArgA 34
|||||
21175 TCCAGGCTATCCCTCCAGACATGCCATGCCCTGAGAAAGAGAGCAAGA 21126
34 rGArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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51 PheGlyGluTyrGlySerTyrValValAspIlePheThrLeuValAs 67
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67 pThrLysTyrPArgHisMetPheValIlePheSerLeuSerTyrIleLeu 84
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84 eTrrPleuIlePheGlySerValPheTrrPleuIleAlaPheHisLysGly 100
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20976 TCCGGTGAATTTGGCTCCATATTTTGGTC.ATACCTTTCATCAGCA 20928
101 .AspLeuLeuAsnAspProAspIleThrProCysVal.AspsnValHis 116
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20927 AACCTATTAAACGATCCAGATATCACCCCTGTGTGGACAAACGGCAT 20878
117 SerPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGly 133
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20877 TCATTTACGCGTCGATTTTATTCTCCCTGGAGACCACCAACCCATTGG 20828
133 TyrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetY 150
|||||
20827 ATACGGTATACCGCTGTGTCACGGAAGAGTCTGTGGCTGATCAGCAG 20778
150 AlIleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGly 166
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20777 TCATCCTTCAGTCCATCCCTCAGCTGCATCAACACCTTCATCATTTGA 20728
167 AlaAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleAr 183
|||||
20727 GCAGCCTTGCCAAAGATGGCAACTGCCCGGAAGAGAGCCACAGCATAG 20678
183 gPheSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuM 200
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20677 CTTACAGCTATTTTGGCCCATTTGATAGAGAGCGGGAAGCTTTGCCCTCA 20628
200 eTrrPArgIleGlyAspPheArgProAsnHisValValIleGluThrVal 216
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20627 TGTGGGCGCATAGTACTTCCGACCAACCATGTGTAGAGGCGCAGGTG 20578
217 ArgAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMe 233
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233 tAlaPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrP 250
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20527 GCGGTTTAAAGACCTCAAACTGTCATATGACCAAGATAATCCTGGTACTTC 20478
250 rValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeu 266

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20427 GACCCGAAAGCAGTGGCCCAAGATTAATTTTCGAGATTTCTGTGACATTTAT 20378
283 eTyrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrV 300
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20377 TTATACTGTGATTCACATCGGGACATCCACCAAGTGCATGCTCTTACA 20328
300 aLProArg**IleLeuTrrGlyHisArgPheAsnAspValLeuVal 316
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317 LysArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValG 333
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333 uValTyrAlaProPheCysSerAlaLysGlnLeuAspTrrLysAspGlnG 350
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20177 AACTCAACAACCTTGGAGAAACGTCCCTGCCCGAGAGATCTGCAATTTCT 20128
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DEFINITION Anguilla japonica mRNA for ekir, complete cds.
ACCESSION AB009669
VERSION AB009669.1 GI:4630767
KEYWORDS ekir.
SOURCE
ORGANISM Anguilla japonica cDNA to mRNA.
Anguilla japonica
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
Anguillidae; Anguilla.
REFERENCE
1 (sites)
AUTHORS Suzuki,Y., Itakura,M., Kashiwagi,M., Nakamura,N., Matsuki,T.,
Sakuta,H., Naito,N., Takano,K., Fujita,T. and Hirose,S.
Identification by differential display of a hyperonclicity-inducible
inward rectifier potassium channel highly expressed in chloride
cells
JOURNAL J. Biol. Chem. 274 (16), 11376-11382 (1999)
MEDLINE 99214223
REFERENCE
2 (bases 1 to 1119)
AUTHORS Suzuki,Y.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1997) Yoshiro Suzuki, Tokyo Institute of
Technology, Department of Biological Sciences, 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:yosuzuki@bio.titech.ac.jp, Tel:81-45-924-5726,
Fax:81-45-924-5824)
FEATURES
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KSHLVEAHRAQLKSRIITVSEGEYIPLDIDINQFDSGIDRIPLVSPITVHEIDED
SPLDLSKODMADFEIIVLEGVATEAMTQCRSSYLANEILMGHRYEPLVEEK
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US-09-623-304A-1 x AF021141 ..

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Align seg 1/1 to: AF021141 from: 1 to: 1284

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118 AGGCACAGATGCGAGAGCCGCTTGTCAAAAGATGGCCACGCAACGT 167
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168 CCAATTATTAAATG...GGTGAAGAGGACACGCACTACCTCGCAGACA 214
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61  LephThrTrPheLeuValAspTrHisTrArgHisMetPheValLLePhe 77
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215 TCCTTCACACACTTCGCTGGACATCCGCTGGAGGTGATGCTGTTATCTTC 264
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78  SerLeuSerTrLLeuSerTrPheLLePheGlySerValPheTrPle 94
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265 TGCCTGACATTCATCCTCTCTGGCTTTCTTGCGTGTTGGTT 314
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94  uLLeAlaPheHisHisGlyAsPheLeuAsnAspProAspLLeThrProc 111
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315 GATTGGCGCTGTGACGGGATCTGGAGAACAAATACAAACCGT 364
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415 ACCCAGACCCAGATCGGCTATGGCTTCAGGTGCGTCACAGATGAGTGCCC 464
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144 rValAlaValLeuMetValLLeuGlnSerLLeuLeuSerCysLLeuLea 161
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465 CATTTGCTGTTTCATGTGTTTCCAGTCTATAGAGGCTCATCATTTG 514
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161 snrPheTrLLeIleGlyAlaAlaLeuAlaLysMetAlaThrAlaArgLys 177
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515 AGCCTTCATCATTTGGTGGCGTATGCGCAAGATGCGCTAAGCCCAAAAAG 564
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178 ArgAlaGlnThrLLeaArgPheSerTrPheAlaLeuLLeGlyMetArgAs 194
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565 AGAAACGAAACCTTGCTTCACGCAAAATGCGGTGGTGCCATGAGAGA 614
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194 pGlyLysLeuCysLeuMetTrPArgLLeGlyAspPheArgProAsnHisY 211
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211 aLValGluGlyThrValArgAlaGlnLeuLeuArgTrThrGluAspSer 227
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665 TGGTTGAGGCACAGTGGCGAGCACAGCTCTCAAGTCCAGGATCACGCTCA 714

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243 .....AspGlnLLeLLeuValThrProValTr 252
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269 LysAlaValAlaLysAspAsnPheGluLLeuValThrPheLLeTrTh 285
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285 rGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTrValProa 302
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903 GGTGAAGCCCTGCCATGACTACCCAGTCCGCGAGCTCATCTAGTGGCAA 952
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302 rg***LLeuTrPglYHisArgPheAsnAspValLeuGluValLysArg 318
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953 ATCAAAATCCTCTGGGCGCACCGCTATGAGCCTTACTCTTTGAAGAAAA 1002
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319 LysTrYTrLysValAsnCysLeuGlnPheGluGlySerValGluVal.. 334
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1003 AACTACTACAAAGTGGACTATTCAGAGTTCCACAAAACATACGAAGTGCC 1052
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335 .TyrAlaProPheCysSerLAlaLysGlnLeu 344
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Ratio: 5.293 Gaps: 0  
Percent Similarity: 99.739 Percent Identity: 99.739

## alignment\_block:

US-09-623-304A-1 x AA221041 ..

Align seg 1/1 to: AA221041 from: 1 to: 1509

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17 rProGlyTyrProGluHisIleIleAlaGluLysArgArgAlaArg 34
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96 CCCAGGCTACCCGCCAGAGACATTTAGCTGAGAGAGAGACAGCAAGA 145
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34 rArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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146 GACGATTACTTCACAAAGATGGCAGCTGTAATGCTTACTTCAAGCAATT 195
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51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67
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196 TTGGAGATGGGGAAGCTATGTGTTGACATCTTCACCACTTTGTGGA 245
|||||
67 pHisTyrTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeus 84
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246 CACCAAGTGGCGCCAAATGTTGTGATATTCTTATCTTAATATCTCT 295
|||||
84 eTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisIleGly 100
|||||
296 CGGTGTTGATTTGGCTCTGCTTTGGCTCATAGCTTTTCATCAGG 345
|||||
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
|||||
346 GATCTATTAAATGATCCAGACATCACACCTTGTTGACAACTCCATTC 395
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117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrIleGlyT 134
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396 TTTCACAGGGGCTTTTGTCTCCCTAGAGCCAAACACCATATGAGAT 445
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134 yGlyTyrArgCysValThrGluGluCysSerValAlaValIleuMetVal 150
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446 ATGCTTATGCTGTGTACTGAGAAATGTTCTGTGGCGCTCATAGGTG 495
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151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
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267 ParGlyAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
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367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSerTrp 383
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1146 CAAGGCGAGACGAAGGTCAATTGTGACAGTTCGCAATGTTCAGCAGCTGG 1194
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seq_name: /SIDSL/gcdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF85049
seq_documentation_block:
ID AAF85049 standard; DNA; 1257 BP.
XX
AC AAF85049;
XX
DF 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of a human Kir5.1 polypeptide.
XX
KW Kir5.1; inwardly rectifying potassium channel; ion channel;
KW renal failure; hypokalemia; hypertension; hypotension; thyroid disease;
KW pancreatitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1257
FT /tag= a
FT /product= "Kir5.1"
XX
WO200125258-A1.
XX
PD 12-APR-2001.
XX
PE 29-SEP-2000; 2000WO-US26996.
XX
PR 04-OCT-1999; 99US-0157491.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Swanson RJ, Liu Y, McKenna E;
XX
WP1: 2001-290604/30.
XX
DR P-PSDB; AAB68275.
XX
PT Novel nucleic acid encoding human Kir5.1 subunit protein useful for
PT identifying activators and inhibitors of potassium channels containing
PT the protein subunit useful for treating various diseases

```

xx Claim 3: Fig 1: 52pp: English.

PS The present sequence encodes a human Kir5.1 subunit protein. Kir5.1  
 CC is an inwardly rectifying potassium channel subunit. Kir5.1 proteins  
 CC are useful for identifying inhibitors or activators of potassium  
 CC channels. Kir5.1 proteins are useful as attractive targets for drug  
 CC discovery and as valuable research tools for understanding ion channel  
 CC biology. Kir5.1 proteins are also useful for identifying inhibitors or  
 CC activators of potassium channels. Inhibitors or activators screened  
 CC using Kir5.1 protein are useful for treating a variety of diseases  
 CC involving excessive or insufficient potassium channel activity, such as  
 CC renal failure, hypokalemia, hypertension, hypotension, thyroid disease  
 CC and pancreatitis.

50 Sequence 1257 BP; 358 A; 287 C; 276 G; 336 T; 0 other;

#### alignment\_scores:

Quality: 2011.00 Length: 382  
 Ratio: 5.278 Gaps: 0  
 Percent Similarity: 99.738 Percent Identity: 99.738

#### alignment\_block:

US-09-623-304A-1 x AAF85049

Align seg 1/1 to: AAF85049 from: 1 to: 1257

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51 CCCAGGCTACCCGCCAGACACATTTATAGCTGAGAGAGAGAGAGAGAA 100
34 rArgIleuIleuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
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51 PheGlyGluTyrPglySerTyrValValAspIlePheThrIleuValAs 67
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67 pThrIysTyrArgHisMetPheValIlePheSerLeuSerTyrIleuAs 84
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201 CACCAAGTGGCGCATATGTTGTGATATTTCTTATCTTATATATCTCT 250
84 eTrrPleuIlePheGlySerValPheTrrPleuIleAlaPheHisIleGly 100
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101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
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301 GATCTATTAATGATCCAGACATCACACCTTGTGTGACAAACGTCATTC 350
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451 ATCTCCAGTCACWCTTAAGTGCATCATTAATACCTTTATCATTTGAGGC 500
167 aaAlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgp 184
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501 TGCCTTGGCCAAATGGCAACTGCTCGAAAGAGGCCCAACCATTCGTT 550
184 heSerTyrPheAlaIleuIleGlyMetArgAspGlyLysLeuCysLeuMet 200

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267 pArgLysAlaValAlaLysAspAsnPhelGluIleLeuValThrPheIleT 284
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901 CCCGAGAAATTTCTGTGGGCGCATAGGTTTAAATGATGCTTGAAGTTAA 950
317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
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1051 CTCACATATGAAAAAGCACCCAGCTTCGAGAAATCTGACAGCTGGACAC 1100
367 rLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
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1101 CAAGCGACAGCAAGATGATTTAGTGACAGTTGCCATTTGTCAGCAGC 1146
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seq_documentation_block:
ID AA592631 standard; cDNA; 1395 BP.
XX
AC AA592631;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #28435.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
  food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001: 2001WO-US08631.
XX
PR 31-MAR-2000: 2000US-0540217.
PR 23-AUG-2000: 2000US-0649167.
XX
PA (HYSB-) HYSB INC.

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PI	Drmanc RT,	Liu C,	Tang YF.
XX	WP1; 2001-639362/73.		
DR	P-PSDB; ABG28444.		
XX	New isolated polynucleotide and encoded polypeptides, useful in		
PT	diagnostics, forensics, gene mapping, identification of mutations		
PT	responsible for genetic disorders or other traits and to assess		
PT	biodiversity -		
XX	Claim 1; SEQ ID No 28435; 103pp; English.		
PS			
XX	The invention relates to isolated polynucleotide (I) and		
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,		
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome		
CC	and gene mapping, and in recombinant production of (II). The		
CC	polynucleotides are also used in diagnostics as expressed sequence tags		
CC	for identifying expressed genes. (I) is useful in gene therapy techniques		
CC	to restore normal activity of (II) or to treat disease states involving		
CC	(II). (II) is useful for generating antibodies against it, detecting or		
CC	quantitating a polypeptide in tissue, as molecular weight markers and as		
CC	a food supplement (II) and its binding partners are useful in medical		
CC	imaging of sites expressing (II). (I) and (II) are useful for treating		
CC	disorders involving aberrant protein expression or biological activity.		
CC	The polypeptide and polynucleotide sequences have applications in		
CC	diagnostics, forensics, gene mapping, identification of mutations		
CC	responsible for genetic disorders or other traits to assess biodiversity		
CC	and to produce other types of data and products dependent on DNA and		
CC	amino acid sequences. AAS64197-AAS94564 represent novel human		
CC	diagnostic coding sequences of the invention.		
CC	Note: The sequence data for this patent did not appear in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
XX	Sequence 1395 BP; 410 A; 319 C; 299 G; 367 T; 0 other;		
Seq			
Alignment_scores:			
	Quality: 2011.00	Length: 382	
	Ratio: 5.278	Gaps: 0	
	Percent Similarity: 99.738	Percent Identity: 99.738	
alignment_block:			
US-09-623-304A-1 x AAS92631 ..			
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17 rProGIYTrPrOProGIunHISileIleAlaGluLysARgALaArGA 34			
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84 eTrTPLeuIlePheGLySerValPheThrPLeuIleAlaPHeNISHISly 100			
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101 AspleuLeuaAnASPProAspIleThrProcysValAlaspsnValInHisse 117			

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134 YrGlyYrThrGlyValThrGluGlyCysSerValAlaValIleMetVal 150  
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seq\_name: /SIDSL/gcgdata/hold-geneseq/gene-seq-emb1/NA2001A.DAT:AAD09566

XX 10-SEP-2001 (first entry)

DE Human transporter and ion channel-15 (TRICH-15) cDNA.

XX Human; transporter and ion channel-15; TRICH-15; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; epilepsy; vaccine; arrhythmia; dementia; depression; ischemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; noctropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 22..1383

FT /tag= a

FT /product= "Human TRICH-15 protein"

FT sig\_peptide 22..117

FT /tag= b

FT mat\_peptide 118..1380

FT /tag= c

FT /product= "Mature human TRICH-15 protein"

XX WO200146258-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000MO-US35095.

XX 23-DEC-1999; 99US-0172000.

PR 14-JAN-2000; 2000US-0176083.

PR 21-JAN-2000; 2000US-0177332.

PR 28-JAN-2000; 2000US-0178572.

PR 02-FEB-2000; 2000US-0179758.

PR 10-FEB-2000; 2000US-0181625.

XX (INCYTE GENOMICS INC.

XX Baughn MR, Burford N, Au-Young J, Lu DAM, Yang J, Reddy R, Lal P, Hillman JL, Azimzai Y, Yue H, Nguyen DB, Yao MG, Gandhi AR, Tang YF, Khan FA;

XX MPI: 2001-418042/44.

DR P-PSDB; AAB04902.

XX Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological disorders -

XX Claim 5; Page 150-151; 160pp; English.

XX The present sequence is transporter and ion channel-15 (TRICH-15) cDNA. TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease, Duchenne muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, muscle disorder including cardiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies,

CC anaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary artery stenosis, Grave's disease, Cushing's disease, Addison's disease, glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic purposes.

XX

XX Sequence 1730 BP; 520 A; 358 C; 361 G; 491 T; 0 other;

XX

alignment\_scores:

Quality: 2011.00 Length: 382

Ratio: 5.278 Gaps: 0

Percent Similarity: 99.738 Percent Identity: 99.738

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127 ATGAGCTATTACGCGACACCTATCATATTATCATCCGCAACCAATA 176

17 rProGlyTyrProProGluHisIleIleAlaGluLysArgAlaArgA 34

177 CCCAGGCTACCCGCCAGACACATTTATAGTGAAGAAGCAAGCAAGA 226

34 rGArGLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50

227 GACGATTACTTTCACAAAGATGCGAGCTGATATGTTACTTCACTCAAGCATT 276

51 PheGlyGluTyrPLeuGlySerTyrValIleAspIlePheThrLeuValas 67

277 TTGGAGAAATGGGGAAGCTATGTTGACATCTTACCCACTCTTGGA 326

67 pThrLysTyrPArgHisMetPheValIlePheSerLeuSerTyrIleLeus 84

327 CACCAAGTGCGCCCATATGTTGATATTTCTTATCTTAATATTCCT 376

84 eTrPLeuIlePheGlySerValPheTrPLeuIleAlaPheHisIleGly 100

377 CGTGTTGATATTTGGCTCTGCTCTTTGGCTCATAGCTTTTCATGATGC 426

101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117

427 GATCTATTAAATGATCCAGACATCACACCTTGTGTGACCAACGTCATTTC 476

117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134

477 TTTTCACAGGGGCTTTTGTTCCTCCATAGACCCAAACACCATAGGAT 526

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527 ATGCTTATCCCTGTGTACTGAAAGAAATGTTCTGTGGCCGCTCATGGTG 576

151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167

577 ATCCCTCAGACCATCTTAAGTTCATCATCATTAATACCTTTATCATGGAGC 626

167 aaIleAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184

627 TGCCTTGGCCAAATGCAACTCTCGAAAGAACGCCAAACCATTCGTT 676

184 heSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200

677 TCAGACTACTTTCGACTTATAGATGATGAGATGGAAAGCTTTGCCCTCATG 726

201 TrPArgIleGlyAspPheArgProAsnHisValIleGluGlyThrValAr 217

727 TGGCGATTGGTGTATTTTGGCCAAACCAACGCTGTGAAGAGAACAGTTAG 776

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1127 TATATGCCCCCTTTTGCAAGTCCAAACATTTGACGGAAGACCGCAG 1176
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ID AAK05088 standard; DNA; 1921 BP.
AC AAK05088;
XX
XX 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 5079.
XX
XX Human: brain expressed exon; gene expression analysis: probe:
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX
XX Homo sapiens.
XX
XX MO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
```

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XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains -
XX
PS Example 4; SEQ ID NO: 5079; 650pp + Sequence Listing; English.
PS
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention.
XX
S0 Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;

alignment_scores:
Quality: 2011.00 Length: 382
Ratio: 5.278 Gaps: 0
Percent Similarity: 99.738 Percent Identity: 99.738

alignment_block:
US-09-623-304A-1 x AAK05088 ..

Align seg 1/1 to: AAK05088 from: 1 to: 1921

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17 rProGlyTyrProProGluHisIleIleAlaGluLysArgAlaArgA 34
|||||
385 CCCAGGCTACCCGCCAGACACATTATAGCTGAGAGAAAGACAAAGAA 434
34 rArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
|||||
435 GACGATTACTTCACAAAGATGCGCAGCTGTAATGTCTACTTCAAGCAT 484
51 PhgGlyGluTyrGlySerTyrValValAspIlePheThrThrLeuValAs 67
|||||
485 TTTGGAGAAATGGGGAAGCTATGAGTTGACATCTTCACCACTGTGTGA 534
67 pThrLysTTPArgHisMetPheValIlePheSerLeuSerTyrIleLeuAs 84
|||||
535 CACCAAGTGGCGCCATATGTTGTGATATTCTTATATCTTATATCTCT 584
84 eTyrPheLeuPheGlySerValPheTyrPheIleAlaPheHisHisGly 100
|||||
585 CGTGCTGATATTGGCTCTGCTCTTTGGCTCATACCTTTATCATGAGC 634
635 GATCTATTAAATGATCCACACATCACACCTGTGTGACAAAGCTCATTC 684
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
|||||
685 TTTTCACAGGGGCTTTTGTCTCCCTAGAGACCAAAACACCATAGGAT 734
134 yArgIlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
|||||
735 ATGCTTATGCGTGTGTACTGAAGAAATGTTCTGTGGCCGCTCATGAGG 784
151 IleuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
|||||
785 ATCTCTCAGCTCATCTTAAGTTGACATCAATAATACCTTATCATTTGAG 834
167 AlaIleuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleAsp 184
|||||
```

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835 TGCCTTGCCAAATGCGCACTGCTGCAAGAGAGAGCCCAACATCTGTT 884
184 heserTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
|||||
885 TCAGCTACTTTCCTTATAGATGATGAGAGATGGAAGCTTTGCCCTCATG 934
201 TTPArgIleGlyAspPheArgProAsnHisValAlaGluGlyThrValArg 217
|||||
935 TGGGCAATGATGATTTTCGCGCAACACCGTGGATAGAGAACAGATTAG 984
217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMet 234
|||||
985 AGCCCAACTTCTCCGCTATACAGAGACAGTGAAGGAGAGATGACGATGG 1034
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|||||
1035 CATTAAAGACCTCAAAATAGTCAACGACCAACAAATCATCTGGTCAACCCG 1084
251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
|||||
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1135 CCGCAAGCAGTAGCCAAAGATACCTTGAGATTGTTGTGACATTATATCT 1184
284 yThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
|||||
1185 ATACTGTGATTCACATGGAACATCTCACAAATCTAGAACGTCCTATGTT 1234
301 ProArg**IleLeuTyrGlyHisArgPheAsnAspValLeuGluValVal 317
|||||
1235 CCCGAGAAATTCCTCTGGGCCATAGSTTTAATATATCTTTGGAAGTTAA 1284
317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGlu 334
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1285 GAGGAAGTATTACAAAGTGAACCTCTTACAGTTTGAAGGAAGTGTGGAAG 1334
334 aLysAlaProPheCysSerAlaLysGlnLeuAspTyrLysAspGlnGln 350
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1335 TATATGCCCCCTTTTGCAAGTCCAAAGCAATTCGCTGGAAGACCAACAG 1384
351 LeuHisIleGluLysAlaProValArgLysCysThrSerSerAspThr 367
|||||
1385 CTCACACATGAAAAAGCACCAACAGCTTCGAAATCCCTGCACGTGGACAC 1434
367 rLysAlaArgArgSerPheSerAlaValAlaIleValSerSer 382
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1435 CAAGGCGAGAGCAAGGTCATTTAGTGCAGTTGCCATTGTCCAGCAGC 1480
seq_name: /stids1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AA136580
seq_documentation_block:
ID AA136580 standard; DNA; 1921 BP.
XX
AC AA136580;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #5266 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
OS genetic disorder; ss.
XX
Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312.

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PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX MPI; 2001-488897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human placenta -
XX
XX Claim 25; SEQ ID No 5266; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 1921 BP; 573 A; 386 C; 395 G; 567 T; 0 other;

```

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alignment_scores:
  Quality: 2011.00      Length: 382
  Ratio: 5.278          Gaps: 0
Percent Similarity: 99.738  Percent Identity: 99.738

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alignment_block:
US-09-623-304A-1 x AA136580 ..

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Align seg 1/1 to: AA136580 from: 1 to: 1921

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1 MetSerTyrTrpGlySerSerTyrHisIleIleAsnAlaAspAlaLysTyr 17
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335 ATGAGCTATTACGGCAGCAGCTATCATATATATCATATGCGGCGCAAAATA 384
17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArg 34
|||||
385 CCCAGGCTACCCGCCAGACGACATATATAGCTGAGAACGAGAACAGAA 434
34 rGArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
|||||
435 GACCATTTACTTTCACAAAGATGGCAGCTGATATGCTTACTTCACACACATT 484
51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrIleValAs 67
|||||
485 TTGGAGAAATGGGGAGAGCTATGTGTGACATCTTCACCACTCTTGGA 534
67 rThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeu 84
|||||
535 CACCAAGTGGCGCATATGTTGTGATATTTCTTATCTTATATTTCTCT 584
84 eTrpIleuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
|||||
585 CGNGTGTGATATTTGGCTCTGTCCTTTGGCTCATAGCCTTTCATCATG 634
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHis 117
|||||
635 GATCTATTAATATGATCCAGACATCACACCTTGTTGTGACAAACGCTTC 684
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|||||
167 aAlaLeuAlaIysMetAlaThrAlaArgIysArgAlaGlnThrIleArgp 184
|||||
835 TGCCTTGGCCAAATGGCAACTGCTGAAAGAGAGCCCAAAACCATTCGCTT 884
|||||
184 heSerTyThrPheAlaLeuIleGlyMetArgAspGlyLysLeuSerLeuMet 200
|||||
885 TCAGACTACTTTCACCTTATAGATAGATGAGATGGAGAGCTTTCCTCATAG 934
|||||
201 TTPArgIleGlyAspPheArgProAsnHisValaIleGlyThrValar 217
|||||
935 TGGCCGATTGGATTTTCGGCCAAACCAAGCTGTAGAGAACACTGTAG 984
|||||
217 gAlaGlnLeuLeuArgTyThrGlnAspSerGlnGlyArgMetThrMetA 234
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985 AGCCCAACTTCTCCGCTATACAGAAAGACAGTGAAGGAGATGACGATGG 1034
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234 lAPheLysAspLeuLysLeuValaAsnAspGlnIleIleLeuValThrPro 250
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1035 CATTTAAACCTCAATATAGTACAGACCAATATCTCTGTCACCCG 1084
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251 ValThrIleValHisGlnIleAspHisGluSerProLeuTyThrAlaLeuAs 267
|||||
1085 GAAACATATGTCATGAAATTCGACATGAGAGCCCTCTGATCCCTTGA 1134
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1185 ATACTGTGATTCACATGACATCTCACCACATGAGACGTCTATGTT 1234
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301 ProArg***IleLeuThrPcIyHisArgPheAsnAspValleuGluVally 317
|||||
1235 CCCGAGAAATTCCTCGGGCCATAGTGAATGATGATCTTGGAAGTTAA 1284
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317 sArgLysTyThrTyLysValaAsnCysLeuGlnPheGlnGlySerValGluV 334
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1285 GAGGAAGTATTCAAAGTAGAAGCTGTACAGTTGAAGGAAGTGTGAAG 1334
|||||
334 aTyThrAlaProPheCysSerAlaLysGlnLeuAspTyThrLysAspGlnG 350
|||||
1335 TATATGCCCCCTTTTCAGATGCCAAGCAATTTGACCTGGAAGACGACAG 1384
|||||
351 LeuHisIleGlnLysAlaProProValaArgGluSerCysThrSerAspTh 367
|||||
1385 CTCCACATGAGAAAGAACACCACAGCTTCGAGAAATCCTGCACGTCGGAC 1434
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367 rLysAlaArgArgSerPheSerAlaValaIleValSerSer 382
|||||
1435 CAAGGCGAGACGAGGTCAATTAGTGCATGTGCATGTGCACGACG 1480
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seq\_name: /SIDS1/gcdata/hold-geneseg/genesegn-emb1/NA2001A.DAT:AAF85050  
 seq\_documentation\_block:  
 ID AAF85050 standard; cDNA: 1257 BP.

AC AAF85050;  
 DT 09-JUL-2001 (first entry)  
 DE Nucleotide sequence of a rat Kir5.1 polypeptide.  
 XX Kir5.1: inwardly rectifying potassium channel; ion channel;  
 KW renal failure; hypokalemia; hypertension; hypotension; thyroid disease;  
 KW pancreatitis; ss.  
 XX Ratius sp.  
 OS

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FH Key Location/Qualifiers
FT CDS 1..1257
FT /tag= a
FT /product= "Kir5.1"
FT /note= "no termination codon given"
XX
XX WO200125258-A1.
XX
XX 12-APR-2001.
XX
XX 29-SEP-2000; 2000WO-US26996.
XX
XX 04-OCT-1999; 99US-0157491.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Swanson RJ, Liu Y, McKenna E;
XX
XX WPI; 2001-290604/30.
XX
XX P-PSDB; AAB68277.
XX
XX Novel nucleic acid encoding human Kir5.1 subunit protein useful for
XX identifying activators and inhibitors of potassium channels containing
XX the protein subunit useful for treating various diseases
XX
XX Disclosure; Fig 4A-B; 52pp; English.
XX
XX The present sequence encodes a rat Kir5.1 subunit protein. Kir5.1
XX is an inwardly rectifying potassium channel subunit. Kir5.1 proteins
XX are useful for identifying inhibitors or activators of potassium
XX channels. Kir5.1 proteins are useful as attractive targets for drug
XX discovery and as valuable research tools for understanding ion channel
XX biology. Kir5.1 proteins are also useful for identifying inhibitors or
XX activators of potassium channels. Inhibitors or activators screened
XX using Kir5.1 protein are useful for treating a variety of diseases
XX involving excessive or insufficient potassium channel activity such as
XX renal failure, hypokalemia, hypertension, hypotension, thyroid disease
XX and pancreatitis.
XX
XX Sequence 1257 BP; 325 A; 325 C; 314 G; 293 T; 0 other;
XX

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alignment\_scores:  
 Quality: 1898.50 Length: 383  
 Ratio: 5.036 Gaps: 1  
 Percent Similarity: 98.433 Percent Identity: 93.473

alignment\_block:  
 US-09-623-304A-1 x AAF85050 ..

Align seg 1/1 to: AAF85050 from: 1 to: 1257

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|||||
51 TCCAGGCTATTCCTCCAGAGCATGCCATACCGGAGAAAGAGAGCAGAGA 100
|||||
34 rArgArgLeuLeuHisLysAspGlySerCysAsnValTyThrPheLysHisIle 50
|||||
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51 PheGlyGluThrPcIySerTyThrValaIleAspIlePheThrThrLeuValAs 67
|||||
151 TTTCGGAATGGGGAGCTACATGTTGATATATTCACCACTCTGTGGA 200
|||||
67 pThrLysTyThrArgHisMetPheValIlePheSerLeuSerTyThrIleLeuS 84
|||||
201 TACCAAGTGGCGCCATATGTTGTAGTATTTCTTGTCTTACATCTCT 250
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84 eTrrPleuIlePheGlySerValPheTrrPleuIleAlaPheHisHisGly 100
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251 CTTGTTGATATTCGGCTCCATATTTGGCTCATAGCCCTTCATCAGCA 300
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101 AspleuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
|||||
301 GACCTATTAAAGCGATCCAGACATCACCCCGCTGGAGCAACAGTGCATTC 350
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117 rPhethrGlyAlaPheLeuPheSerLeuGluThrGlnThrIleGlyT 134
|||||
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134 YrGlyTyrArgCysValThrGluGluCysSerValAlaValIleuMetVal 150
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401 ACGGTTACCGCTGTGTGCACGGAAGAAATGCTCTGTGGCCGCTCTACGCTC 450
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151 IleuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
|||||
451 ATCCTTCAGTCCATCTGAGCTGCATCATTAACACCTTCATCATTTGGGCG 500
|||||
167 aaIleuAlaLeuMetAlaThrAlaArgLysArgAlaGlnThrIleArgp 184
|||||
501 AGCCTTGCAAAAGATGGCGAGCCCGGAAAGCGAGCCAGACATCCGCT 550
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184 heserTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
|||||
551 TCAGCTATTTCGCACATCGGCATGAGAGAGCGGAACCTTTGGCTCATG 600
|||||
201 TrrArgIleGlyAspPheArgProAsnHisValAlaGluGlyThrValAr 217
|||||
601 TGGGCGCATAGGTGACTTCGACCGAACCATGTGTGGAGGCGACGAGTAC 650
|||||
217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMet 234
|||||
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701 CGTTTAAAGACCTCAAACTCGTCAATGACACGAAATATCTGTGTAACGCCA 750
|||||
251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
|||||
751 GTGACCTTTCTCCATGAAATTGACACGAGAGTCTGTATGCCCTTGA 800
|||||
267 PaGlyAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
|||||
801 CCGCAAGCGAGTGGCCAAAGATAATTCAGATTCTGTGTCATTTATTT 850
|||||
284 YrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
|||||
851 ATACTGGTGACTCTACTGGGACATCCACACGATCCAGAAATGCTTACTGCTC 900
|||||
301 ProArg**IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLy 317
|||||
901 CCCAGAGAAATTTCTGTGGGACACAGGTTTCATGATGATGGAAGTGA 950
|||||
317 saGlyLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluV 334
|||||
951 GAGAAATGACTACAAAGGTAAACGCTTGCAAGTTTGAGGGGAAGCCTGGAG 1000
|||||
334 alTyrAlaProPheCysSerAlaLysGlnLeuAspTrrPlysAspGlnGln 350
|||||
1001 TCTACGCCCTTTTTCAGATGCCAAACACATCGCATGAGAGACCAACAG 1050
|||||
351 Leu...HisIleGluLysAlaProProValArgLysCysThrSerAs 366
|||||
1051 CTCMAACAACCTTGGAGAAAGCTCCCTGCGCCAGAGATCTGACACCTCGGA 1100
|||||
366 pThrLysAlaArgArgArgSerPheSerAlaValAlaIleValSerSer 382
|||||
1101 CACCACACACAGGAGGAGATCTTTCACGCGCAGTTGTCATGGTGAGAGC 1149
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seq_documentation_block:
ID      AAK17807 standard; DNA; 1118 BP.
XX
AC      AAK17807;
XX
DT      05-NOV-2001 (first entry)
XX
DE      Human brain expressed single exon probe SEQ ID NO: 17798.
XX
KW      Human: brain expressed exon; gene expression analysis; probe;
KW      microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW      epilepsy; cancer; ss.
XX
OS      Homo sapiens.
XX
PN      WO200157275-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001: 2001WO-US00667.
XX
PR      04-FEB-2000: 2000US-0180312.
PR      26-MAY-2000: 2000US-0207456.
PR      30-JUN-2000: 2000US-0608408.
PR      03-AUG-2000: 2000US-0632366.
PR      21-SEP-2000: 2000US-0234687.
PR      27-SEP-2000: 2000US-0236359.
PR      04-OCT-2000: 2000GB-0024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR:
XX
DR      WPI; 2001-483446/52.
XX
PT      Single exon nucleic acid probes for analyzing gene expression in human
PT      brains -
XX
PS      Example 4; SEQ ID NO: 17798; 650bp + Sequence Listing; English.
XX
PS      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CC      which may enable the diagnosis and improved treatment of nervous system
CC      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC      epilepsy and cancers. The present sequence is one of the probes of the
CC      invention.
XX
SQ      Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;

alignment_scores:
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      Ratio: 5.300      Gaps: 0
Percent Similarity: 99.707      Percent Identity: 99.707

alignment_block:
US-09-623-304A-1 x AAK17807 ..

Align seg 1/1 to: AAK17807 from: 1 to: 1118

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17 rProGlyTyrzProProGluHisIleIleAlaGluLysArgTrgaLaArga 34
|||||
144 CCCAGGCTACCCGCCAGAGCAGCATTTATAGCTGAGAAAGAGAGACAGAA 193
|||||
34 rGArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
|||||
194 GACGATTACTTACCAAGAGATGGCAGCTGTATATGTCTACTTCAACACAT 243

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51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67  
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67 pThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeuS 84  
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294 CACCAAGTGGCCGCAATAGTTGTGATATTTCTTATCTTATATTTCT 343  
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344 CGTGGTGTGATATTGGCTGTGCTTTGGCTCATAGCCTTTCATCATG 393  
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544 ATCTCCAGTCCACTTAAGTTCATCATTAATACCTTATCATTTGGAG 593  
167 AlaLeuAlaLysMetAlaThrAlaArgLysArgAlaGlnThrIleArg 184  
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594 TGCTTGGCCAAATGGCACTGCTCGAAAGAGAGCCCAACCATTCGT 643  
184 hSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200  
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644 TCAGCTCACTTGCACCTTATGATGAGATGGGAAGCTTTCCTCATG 693  
201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrVal 217  
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694 TGCGCATTTGCTGATTTTGGCCAAACCACTGTGTGAGAAAGAGTGA 743  
217 GAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgMetThrMe 234  
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317 sArgLysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGlu 334  
|||||  
1044 GAGGAAGTATTACAAAGTGAACGTCTTACAGTTTGAAGAGAGTGTGA 1093  
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seq\_documentation\_block:  
ID AA149699 standard; DNA; 1118 BP.

AC AA149699;  
XX  
DT 17-OCT-2001 (first entry)  
XX

DE Probe #18385 used to measure gene expression in human placenta sample.

XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder; ss.  
XX

OS Homo sapiens.  
XX

PN W0200157272-A2.  
XX

PD 09-AUG-2001.  
XX

XX 30-JAN-2001; 2001WO-US00663.  
PF

XX 04-FEB-2000; 2000US-0180312.  
PR

PR 26-MAY-2000; 2000US-0207456.  
PR

PR 30-JUN-2000; 2000US-0608408.  
PR

PR 03-AUG-2000; 2000US-0632366.  
PR

PR 21-SEP-2000; 2000US-0234687.  
PR

PR 27-SEP-2000; 2000US-0236359.  
PR

PR 04-OCT-2000; 2000GB-0024263.  
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX

DR WPI; 2001-488897/53.  
XX

XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human placenta -

XX Claim 25; SEQ ID No 18385; 654bp; English.  
XX

XX The present invention relates to single exon nucleic acid probes (SENP).  
CC The present sequence is one such probe. The probes are useful for  
CC producing a microarray for predicting, measuring and displaying gene  
CC expression in samples derived from human placenta. The probes are useful  
CC for antenatal diagnosis of human genetic disorders.  
XX

XX Sequence 1118 BP; 320 A; 250 C; 239 G; 309 T; 0 other;  
SQ

alignment\_scores:  
Quality: 1802.00 Length: 341  
Ratio: 5.300 Gaps: 0  
Percent Similarity: 99.707 Percent Identity: 99.707

alignment\_block:  
US-09-623-304A-1 x AA149699 ..

Align seg 1/1 to: AA149699 from: 1 to: 1118

1 MetSerTyrTyrGlySerSerTyrHisIleIleAsnAlaAspAlaLysTyr 17  
|||||  
94 ATGAGCTATTACGGCAGCAGCTATCATATTATTCATATGCGGACGCAATA 143  
17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArg 34  
|||||  
144 CCGAGGCTACCCGCCAGACACATTTATACCTGAGAAAGAGACGACAGA 193  
34 rArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50  
|||||  
194 GACGATTACTTCACAAAGATGCGAGCTGTAATGTCTACTTCAAGCACAT 243  
51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValAs 67  
|||||

```

244 TTGGAGAAATGGGAGAGCTATGGTGGTACATCTTCACCACTCTTGCTGA 293
XX
67 pThyStrpAtrghIsmetPheValIlePheSerLeuSerTyrIleLeuS 84
|||||
294 CACCAAGTGGGCGCATATGTTTGATATTTCTTTATCTTATATATCTCT 343
84 erTrpLeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGly 100
|||||
344 CGTGGTGGATATTTGGCTCTGCTTTGGCATATAGCCTTTCATCATATGCG 393
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
394 GATCTATTAATGATCCAGACATCACACCTTGTTGCAACGTCATTC 443
117 rPheThrGlyAlaPheLeuPheSerLeuGluThrGlnThrThrIleGlyT 134
|||||
444 TTTCACAGGGGCTTTTGTCTCCCTAGAGACCACCAACCATAGAT 493
134 YrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVal 150
|||||
494 ATGGTATTCGCTGTGTACTAGAGATTTCTGTGGCCGCTCATGTG 543
151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
|||||
544 ATCCCTCAGTCCATTTAAGTTCATCATTAATACCTTTATCATTTGAGC 593
167 aAlaLeuAlaIysMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
|||||
594 TGCCTTGGCCAAATGCGACACTGCGAAGAGAGCCCAACCATCTCTT 643
184 heserTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
|||||
644 TCACCTACTTTGCACCTATAGTATGAGAGATGGAGACTTGCCTCATG 693
201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
694 TGGCGCATTTGGTGAATTTCCGGCCAAACCATGCTGTAGAAGACAGTTAG 743
217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluGlyArgmethrMetAl 234
|||||
744 AGCCCAACTTCTCCGCTATACAGAGAGAGGAGGAGATGACGAGG 793
234 IapheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
|||||
794 CATTTAAAGACCTCAATTAAGTCAACGACCAATCATCTCTGTCAACCCG 843
251 ValThrIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAs 267
844 GTACTATTTGTCCATGAAATGACCATGAGAGCCCTGTGTATGCCCTTGA 893
267 PaTrpLysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleT 284
894 CCGCAAAAGCACTAGCCAAAGATTAACCTTGAGATTTGGTGACATTTACT 943
284 YrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrVal 300
944 ATATGTGGATTCACACTGGAACATCTCACCAATCTAGAAAGCTCCATGTT 993
301 ProArg**IleLeuTrpGlyHisArgPheAsnAspValLeuGluValLys 317
994 CCCCAGAAATTTCTGTGGGCGCATAGGTTTAATGATGTCCTTGGAAAGTTAA 1043
317 sArgLysTyrTrpLysValAsnCysLeuGlnPheGluGluSerValGluV 334
1044 GAGGAAGATATACAAAGTGAATGCTGTACACTTTGAGAAAGTGTGAGAG 1093
334 aLtyrAlaProPheCysSerAla 341
1094 TATATGCCCTTTTGCAGTGCC 1116
seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAK35738
seq_documentation_block:

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ID AAK35738 standard; cDNA; 765 BP.
XX
AC AAK35738;
XX
DT 09-JUL-1999 (first entry)
XX
DE cDNA encoding a protein identified by the signal sequence trap method.
XX
KW Signal sequence trap method; SST method; immunisation; inhibition;
KW infection; allergy; cancer; regulation; tissue formation; tissue repair;
KW activin activity; inhibin activity; chemokine activity;
KW cytokine activity; blood coagulation regulation; agonist; antagonist;
KW metabolic disorder; hormonal disorder; immune disorder;
KW severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
KW wound; ss.
XX
OS Homo sapiens.
XX
PN MO9918126-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98WO-JP04514.
XX
PR 07-OCT-1997; 97JP-0274674.
XX
PA (ONOX ) ONO PHARM CO LTD.
XX
PI Fukushima D, Shibayama S, Tada H;
XX
DR WPI: 1999-277254/23.
XX
P P-SDB: AAY02380.
XX
PT Polypeptides identified by the signal sequence trap method from a
PS human cDNA library
XX
PS Claim 5; Page 212; 281pp; Japanese.
XX
CC AAX35694-X35747 represent cDNA sequences that encode novel polypeptides
CC (AAY02358-84) which are identified from a human placental cDNA library
CC by the signal sequence trap (SST) method. The polypeptides have a
CC broad range of physiological activity, including immunisation against
CC and inhibition of infections, allergies and cancer; regulation of tissue
CC formation and repair; activin/inhibin activity; chemokine/cytokine
CC activity; blood coagulation regulation; and receptor/ligand agonist
CC or antagonist activity. The polypeptides can be used for prevention
CC and treatment of disorders including infections by bacteria, yeasts and
CC viruses (including HIV) and protozoa; metabolic and hormonal disorders;
CC immune disorders (including severe combined immunodeficiency (SCID)
CC and AIDS; thrombosis; cancer; and traumatic or surgical wounds.
XX
SQ Sequence 765 BP; 206 A; 175 C; 167 G; 217 T; 0 other;
XX
alignment_scores:
Quality: 1343.00 Length: 254
Ratio: 5.287 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-623-304A-1 x AAX35738 ..
Align seg 1/1 to: AAK35738 from: 1 to: 765
1 MetSerTyrTyrGlySerSerTyrHisIleIleAsnAlaAspAlaLysTyr 17
|||||
1 ATGAGCTATTACGGCGACGACGATCATGATTAATGATGCGGACGCAAAATA 50
17 rProGlyTyrProProGlnHisIleIleAlaGluLysArgArgAlaAspG 34
51 CCCAGGCTACCGGCCGAGACACATTATAGCTGAGAAAGAAAGACGCAADA 100
34 rGArgLeuLeuHisLysAspLysSerCysAsnValTyrPheLysHisIle 50

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101 GACCATTTACTTACAAAGATGCGAGCTGTAATGCTACTTCAAGCACATT 150
51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValas 67
151 TTTGAGAAATGGGAGAGCTATGTGTTGACATCTTCAACCATCTGTTGGA 200
67 PThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeus 84
201 CACCAAGTGGGCGCATATGTTGTGATATTTCTTATCTTATATTTCTCT 250
84 eTrPLeuIlePheGlySerValPheTrpLeuIleAlaPheHisIleGly 100
251 CGTGGTTGATTTTGGCTCTCTCTTTGGCTCATAGCCTTTTCATCATAGC 300
101 AspLeuLeuAsnAspProAspIleThrProCysValAspAsnValHisSe 117
301 GATCTATTTAAATGATCCAGACATCACACCTTGTTGACAAAGTCATTC 350
117 rPheThrGlyValAlaPheLeuPheSerLeuGluThrGlnThrIleGlyT 134
351 TTTTACAGGGGCTTTTGTGTTTCTCCCTAGAGACCCAAACCCATAGAT 400
134 YrGlyTyrArgCysValThrGluGlyCysSerValAlaValIleuMetVal 150
401 ATGGTTATCCGCTGTACTACTCAAAATGTTCTGTGGCCGCTCATGCTG 450
151 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGlyAl 167
451 ATCTCCAGTCACATCTTAAGTTGCATCATAAATACCTTTATCATTTGAGC 500
167 AlaIleuAlaIleuMetAlaThrAlaArgLysArgAlaGlnThrIleArgP 184
501 TGGCTTGGCCAAATATGGCACTGCTGAAAGAGAGCCCAACCTTGTGTT 550
184 hSerTyrPheAlaLeuIleGlyMetArgAspGlyLysLeuCysLeuMet 200
551 TCAGCTACTTGGCATATAGTATGAGATGGGAAGCTTTGCTCATG 600
201 TrpArgIleGlyAspPheArgProAsnHisValValGluGlyThrValAr 217
601 TGGCGCATTTGGTATTTTCGGCCAAACACAGTGGTTAGAGAAACAGTTAG 650
217 gAlaGlnLeuLeuArgTyrThrGluAspSerGluArgMetThrMetA 234
651 AGCCCAACTTCTCCGCTATACAGAGACAGTGAAGGAGAGATGCGATGG 700
234 labPheLysAspLeuLysLeuValAsnAspGlnIleIleLeuValThrPro 250
701 CATTTAAAGACCTCAATTTAGTCAACGACCAATCATCTGTCACCCCG 750
251 ValThrIleVal 254
751 GTAACATATTGTCT 762
seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/MA1999.DAT:AAK35739
seq_documentation_block:
ID AAK35739 standard; cDNA: 907 BP.
XX
XX AAK35739;
XX
XX 09-JUL-1999 (first entry)
DE cDNA encoding a protein identified by the signal sequence trap method.
XX
XX Signal sequence trap method: SST method; immunisation; inhibition;
XX infection; allergy; cancer; regulation; tissue formation; tissue repair;
XX cytokine activity; blood coagulation regulation; agonist; antagonist;
XX metabolic disorder; hormonal disorder; immune disorder;
XX severe combined immunodeficiency; SCID; AIDS; thrombosis; cancer;
XX wound; ss.

```

```

XX OS Homo sapiens.
XX PN M0918126-A1.
XX PD 15-APR-1999.
XX PF 06-OCT-1998; 98MO-JP04514.
XX PR 07-OCT-1997; 97JP-0274674.
XX PA (ONOX ) ONO PHARM CO LTD.
XX PI Fukushima D, Shibayama S, Tada H;
XX DR WPI; 1999-277254/23.
XX PT P-PSDB; AAY02380.
XX PS Polypeptides identified by the signal sequence trap method from a
    human cDNA library
XX Claim 4; Page 213-215; 281pp; Japanese.

```

AAK35694-X35747 represent cDNA sequences that encode novel polypeptides (AAI02358-84) which are identified from a human placental cDNA library by the signal sequence trap (SST) method. The polypeptides have a broad range of physiological activity, including immunisation against and inhibition of infections, allergies and cancer; regulation of tissue formation and repair; activin/inhibin activity; chemokine/cytokine activity; blood coagulation regulation; and receptor/ligand agonist or antagonist activity. The polypeptides can be used for prevention and treatment of disorders including infections by bacteria, yeasts and viruses (including HIV) and protozoa; metabolic and hormonal disorders; CC immune disorders (including severe combined immunodeficiency (SCID) CC and AIDS; thrombosis; cancer; and traumatic or surgical wounds.

Sequence 907 BP; 278 A; 210 C; 183 G; 236 T; 0 other;

alignment\_scores:  
 Quality: 1343.00 Length: 254  
 Ratio: 5.287 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-623-304A-1 x AAK35739 ..

Align seg 1/1 to: AAK35739 from: 1 to: 907

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1 MetSerTyrTrpGlySerTyrHisIleIleAsnAlaAspAlaLysTyr 17
|||||
78 ATGAGCTATTACGGCAGCAGCTATCATATTATCAATGCGGAGCAATAATA 127
17 rProGlyTyrProProGluHisIleIleAlaGluLysArgArgAlaArgA 34
128 CCCAGGCTACCCGCCAGACGACATTAATAGCTGAGAGAGAGAGCAAGAA 177
34 rGArgLeuLeuHisLysAspGlySerCysAsnValTyrPheLysHisIle 50
|||||
178 GACGATTTACTTCAAAAGATGGAGCTGTATATGCTTCAAGCACATT 227
51 PheGlyGluTrpGlySerTyrValValAspIlePheThrThrLeuValas 67
228 TTTGAGAAATGGGAGAGCTATGTGTTGACATCTTCAACCATCTGTTGGA 277
67 PThrLysTrpArgHisMetPheValIlePheSerLeuSerTyrIleLeus 84
|||||
278 CACCAAGTGGGCGCATATGTTGTGATATTTCTTATCTTATATTTCTCT 327
84 eTrPLeuIlePheGlySerValPheTrpLeuIleAlaPheHisIleGly 100
|||||
328 CGTGGTTGATTTTGGCTCTGTTTGGCTCATAGCCTTTTCATCATAGC 377

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```

211 aValaGluGlyThrValArgAlaGlnLeuLeuArgTyrTrhGluAspSer 227
    ::::::::::: |||||
665 TGCTAGAAAGCTCATGTCGAGCCAGCTCCTCAAAATCCAGAAATTAATCTCT 714
    ::::::::::: |||||
228 GluGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsn..... 242
    ::::::::::: |||||
715 GAAGGGGAA.....TACATCCCTTGATCAAAATAGACATCAA 752
    ::::::::::: |||||
243 .....AspGlnIleIleLeuValThrProValT 252
    ::::::::::: |||||
753 TGTGGCTTGACAGTGGAAATTCACCTATATTCTTGTTATCCCAATCA 802
    ::::::::::: |||||
252 hrtIleValHisGluIleAspHisGluSerProLeuTyrAlaLeuAspArg 268
    ::::::::::: |||||
803 CTATTGTCATGAATATGATGAAGATAGTCCTTATATGATTGAGACAAG 852
    ::::::::::: |||||
269 LysAlaValAlaLysAspAsnPheGluIleLeuValThrPheIleTyrTh 285
    ::::::::::: |||||
853 CAGGACATGTATATGACAGACTTGAAATGTTGTACTACTAGAGCAT 902
    ::::::::::: |||||
285 rGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrValProA 302
    ::::::::::: |||||
903 GGTGGAAAGCCACTGCCATGCACACACAGTCTCGTATTCTTATTGGCCA 952
    ::::::::::: |||||
302 rgt**1leLeuTrpGlyHisArgPheAsnAspValLeuGluValLysArg 318
    ::::::::::: |||||
953 ACGAGATCCCTTGGGGCCACCGCTATGAGCCAGCTCTTGAGAGAAAG 1002
    ::::::::::: |||||
319 LysTyrTyrLysValAsnCysLeuGlnPheGluGlySerValGluVal.. 334
    ::::::::::: |||||
1003 CACTACTATTAAGTGGACTATTCGAGGTTCATTAAGACTTACGAAATACC 1052
    ::::::::::: |||||
335 .TyrAlaProPheCysSerAlaLysGlnLeu 344
    ::::::::::: |||||
1053 CAACACTCCCTTTGTAGTCCACAGAGACTTA 1083
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA35969
seq_documentation_block:
ID ABA35969 standard; DNA; 1310 BP.
XX ABA35969;
XX
XX 23-JAN-2002 (first entry)
XX
XX DE Probe #14435 for gene expression analysis in human heart cell sample.
XX
XX KW Human; gene expression; heart; microarray; vascular system; probe;
XX KW cardiovascular disease; hypertension; cardiac arrhythmia;
XX KW congenital heart disease; ss.
XX
XX OS Homo sapiens.
XX
XX PN W0200157274-A2.
XX
XX 09-AUG-2001.
XX
XX PD 30-JAN-2001; 2001WO-US000666.
XX
XX PE 04-FEB-2000; 2000US-0180312.
XX
XX PR 26-MAY-2000; 2000US-0207456.
XX
XX PR 30-JUN-2000; 2000US-0608408.
XX
XX PR 03-AUG-2000; 2000US-0632366.
XX
XX PR 21-SEP-2000; 2000US-0234687.
XX
XX PR 27-SEP-2000; 2000US-0236359.
XX
XX PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.

```

```

XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
PT
XX Claim 4; SEQ ID NO 14435; 530pp; English.
PS
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, measuring and displaying gene expression in samples derived
XX from the human heart via microarrays. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging,
XX monitoring and prognosing diseases of the human heart and vascular system
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
SQ Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

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alignment_scores:
    Quality: 827.00      Length: 327
    Ratio: 3.256        Gaps: 5
    Percent Similarity: 77.676    Percent Identity: 51.376

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alignment\_block:

US-09-623-304A-1 x ABA35969 ..

Align seg 1/1 to: ABA35969 from: 1 to: 1310

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29 LysAlaArgAlaArgArgLeuLeuHisLysAspLysCysAsnVa 45
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144 CGACACAGTGCAGAGACCCCTTGTGACAGAAAGATGACCCTGTAATGT 193
    ::::::::::: |||||
45 LTrpPheLysHisIlePheGlyGluTrpGlySer...TyrValAlaAspI 61
    ::::::::::: |||||
194 TCAGTTCATCAATGTG...GGTGAGAGGGGCAACGGTACTCCGACAGACA 240
    ::::::::::: |||||
61 IepheThrTrhLeuValAspTrhLysTrpArgHisMetPheValIlePhe 77
    ::::::::::: |||||
241 TCTTCACACGCTGTGTGACATTCGCGGGGCGAGGATGCTGTTATCTTC 290
    ::::::::::: |||||
78 SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpC 94
    ::::::::::: |||||
291 TGCTGGCTTTCCTGCTGCTGATGCTGCTGTTTGGCTGTGTGTTTGCTT 340
    ::::::::::: |||||
94 uIleAlaPheHisIleGlyAspLeuLeuAsnAspProAspIleThrProC 111
    ::::::::::: |||||
341 GATAGCTCTGCTCATGCGGAGCCTGGATGCATCCAAAGAGGCCAAAGCTT 390
    ::::::::::: |||||
111 yValAspAsnValHisSerPheThrGlyAlaPheLeuPheSerLeuGlu 127
    ::::::::::: |||||
391 GTGTGTCCGAGGTCAACAGCTTCACGCTCCCTTCCTTCATTTGAG 440
    ::::::::::: |||||
128 ThrGlnThrTrhIleGlyTyrGlyTyrArgCysValThrGluGluCysSe 144
    ::::::::::: |||||
441 ACCCAGACAAACCATAGGCTATGGTTTCAGATGTGTGCAGGATAAATGCC 490
    ::::::::::: |||||
144 ValAlaValAlaMetValIleLeuGlnSerIleLeuSerCysIleLea 161
    ::::::::::: |||||
491 AATTGCTGTTTCATGTTGTTGTTCCAGTCAATCGTGGGCTGATCATCG 540
    ::::::::::: |||||
161 snThrPheIleIleGlyAlaAlaLeuAlaLysMetAlaThrAlaArgLys 177
    ::::::::::: |||||
541 ATGCTTTCATCATTTGGCGAGTCATGCGCAAGATGCAAGGCCAAAGAGAG 590
    ::::::::::: |||||
178 ArgAlaGlnThrLeaArgPheSerTyrPheAlaLeuIleGlyMetArgAs 194
    ::::::::::: |||||
591 AGAAAGAGAGCTTGTCTTCAGTCAATGCCGTATGTCCATGAGAGA 640
    ::::::::::: |||||
194 rGlyLysLeuCysLeuMetTrpArgIleGlyAspPheArgProAsnHisV 211

```



```

211 aIvalGluglyThrValArgAlaGlnLeuLeuArgTyrThrGluAspSer 227
    ::::::::::: |||||
691 TGGTGAAGCATGTTGAGACACACCTCTCAATCCAGAAATTACTTCT 740
    |||||
228 GlUGlyArgMetThrMetAlaPheLysAspLeuLysLeuValAsn..... 242
    |||||
741 GAAGGGGAG.....TATATCCCTCTGGATCAATAGACATCA 778
    ::
243 .....AspGlnLeuLeuValThrProValT 252
    |||
779 TGTGGGTTTGACAGTGAATGCATGTATATTCTGGTCCCAATCA 828
    |||
252 hrTLeValHisGluLeuAspHisGlnSerProLeuTyrAlaLeuAspArg 268
    |||||
829 CATATGTCATGAAATAGATGAAGACAGCTTTATATGATTGACTATA 878
    |||||
269 LysAlaValAlaLysAspAsnPheGluTLeuValThrPheIleTyrTh 285
    ::
879 CAGGACATTGACACGACGACCTTTGAAATCGTGCATACTGGAAGCAT 928
    ::
285 rGlyAspSerThrGlyThrSerHisGlnSerArgSerSerTyrValPro 302
    |||
929 GGTGAAGCCTGCTGCATGACGACACAGTCCGTACTCTTATCTAGCA 978
    |||
302 rg***IleLeuTyrPglYHisArgPheAsnAspValLeuGluValLysArg 318
    :: |||||
979 ATGAATATCCTGTGGGCGCACCGCTATGACCGTCTTTGAAGAAGAG 1028
    |||||
319 LysTyrTyrLysValAsnGlyLeuGlnPheGluGlySerValGluVal.. 334
    |||||
1029 CACTACTTCAAAAGTGACATTCACAGTTCACAAAACCTTACGAAGTCCC 1078
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335 TyrAlaProPheCysSerAlaLysGlnLeu 344
    ::|||
1079 CAACACTCCCTTTGTAGTCCAGACACTTA 1109
    |||
seq_name: /SIDS1/gcdata/hold-geneseq/geneseg-emb1/NA2001A.DAT:AA149214
seq_documentation_block:
ID AA149214 standard; DNA; 1310 BP.
XX
AC AA149214;
XX
DT 17-Oct-2001 (first entry)
XX
DE Probe #17900 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
XX
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for

```

```

PT analyzing gene expression in human placenta -
XX
PS Claim 25; SEQ ID NO 17900; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 1310 BP; 354 A; 302 C; 336 G; 318 T; 0 other;

alignment_scores:
    Quality: 827.00      Length: 327
    Ratio: 3.256        Gaps: 5
    Percent Similarity: 77.676      Percent Identity: 51.376

alignment_block:
US-09-623-304A-1 x AA149214 ..

Align seg 1/1 to: AA149214 from: 1 to: 1310

29 LysArgAlaGAlaArgArgLeuLeuHisLysAspGlySerCysAsnVa 45
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144 CGACAACAGTGCAGAGCCGCTTGTGAAGAAAAGATGCCACAGTATGT 193
    |||
45 LyrPheLysHisIlePheGlyGluTyrPglYser...TyrValAlaSpl 61
    |||
194 TCGATTATCATATGTG...GGTGAAGAGGGCAACGCTACCTCGCACGA 240
    |||
61 LephThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
    |||||
241 TCTTACCAACGTGTGTGACATTCGCTGGCGGTGATGCTGTATCTTC 290
    |||||
78 SerLeuSerTyrTLeuSerTyrPleuIlePheGlySerValPheTyrPle 94
    |||
291 TGCCTGGCTTTCCTCCTGCATGCGCTGTTTGTGGCTGTGTGTGCTT 340
    |||
94 UleAlaPheHisHisGlyAspLeuLeuAsnAspProAspIleThrProc 111
    |||||
341 GATAGCTGTCTCATGAGGACCTGGATGCATCCAAAGAGGCCAAGCTT 390
    |||
111 ySValAspAsnValHisSerPheThrGlyAlaPheLeuPheSerLeuGln 127
    |||||
391 GTGTGTCCAGGTGCACACAGCTTCACGGCTTCCTTCTTCCATTTAG 440
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Date: Aug 21, 2002 10:13 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

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-MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200  
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## Search information block:

Query: US-09-623-304A-1  
Query length: 383  
Database: Issued\_Patents\_NA\*  
Database sequences: 383533  
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Search time (sec): 47.100000

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## seq\_documentation\_block:

Sequence 1, Application US/08461690B  
Patent No. 5670335  
GENERAL INFORMATION:  
APPLICANT: Jan, Lily Y.  
APPLICANT: Jan, Yuh Nung  
APPLICANT: Kubo, Yoshinori  
APPLICANT: Reveny, Eitan  
APPLICANT: Slesinger, Paul A.  
TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier  
TITLE OF INVENTION: Potassium Channel CDNAS  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,690B  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/103,445  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-58619-1/WHD/JPB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2310 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
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NAME/KEY: CDS  
LOCATION: 338..1624  
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45  LTrpPheLysHisLeuPheGlyLysTrpGlySer...TyrValValAspI 61
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505  TCAGTTATTCACAGT...GGTGAAGAGGACAGAGGTACCTGGCAGACA 551
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61  LephThrThrLeuValAspThrLysTrpArgHisMetPheValIlePhe 77
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552  TCTTACTACCTGTGTCAGATCCGCTGGAGGTGATGCTGTTATCTTC 601
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78  SerLeuSerTyrIleLeuSerTrpLeuIlePheGlySerValPheTrpLe 94
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602  TGTCTTGCCTTCGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 651
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94  uIleAlaPheHisHisGlyAspLeuLeuAsnAspProAspIleThrProC 111
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652  GATAGCCCTGCTCATGGGATCTAGATCTTAAAGTGAAGCAAGCAT 701
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702  GCGTGTGCGAGGTCAACAGCTTCACGGCTCCCTTCCTTCATCGAG 751
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128  ThrGlnThrThrIleGlyTyrGlyTyrArgCysValThrGluLucySe 144
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752  ACCCAACAACAACCATGTGCTATGGTTTCAGGTGTGTGACAGACGACCC 801
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: Sequence 5, Application US/08614801A
: Patent No. 5744324
: GENERAL INFORMATION:
: APPLICANT: Lester, Henry A.
: APPLICANT: Davidson, No. 5744324man
: APPLICANT: Kofuji, Paulo
: TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
: TITLE OF INVENTION: MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF,
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: United States
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/614,801A
: FILING DATE: 07-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/066,371
: FILING DATE: 21-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Treacartin, Richard F.
: REGISTRATION NUMBER: 31,801
: REFERENCE/DOCKET NUMBER: A-63098/RET
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299

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: INFORMATION FOR SEQ ID NO: 5:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 2301 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: unknown
:     TOPOLOGY: unknown
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: 308..1435
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alignment_block:
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429 CCGACCGTCACGTGACCGACCGTTCACACAGCTGTGACCTGCAGTGG 478

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seq_name: /cgn2.6/prodata/2/lna/5A.COMB.seq:US-08-614-801A-3
seq_documentation_block:
Sequence 3, Application US/08614801A
Patent No. 5744324
GENERAL INFORMATION:
APPLICANT: Lester, Henry A.
APPLICANT: Davidson, No. 5744324man
APPLICANT: Kofuji, Paulo
TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
TITLE OF INVENTION: MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
City: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,801A
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/066,371
FILING DATE: 21-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-63098/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown

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? TOPOLOGY: unknown
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 488..1729
? us-08-614-801A-3

alignment_scores:
    Quality: 730.50      Length: 331
    Ratio: 2.854         Gaps: 5
    Percent Similarity: 77.341    Percent Identity: 41.994

alignment_block:
US-09-623-304a-1 x US-08-614-801A-3 ..

Align seg 1/1 to: US-08-614-801A-3 from: 1 to: 1978

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614 CCGAGACACATCAGCCGACAGACAGCAAAAGAAATCCAGAGGTACGT 663
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37 UHSLysASpGlySerCysAsnValTYrPheLysHisIlePheGlyLut 54
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664 GAGGAGGATGGAGAGTGCACACGTTCCACGCGCATGTG...CGGAGA 710
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54 rpgLyseryValValAspIlePheThrThrLeuValAspThrLysTrp 70
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71 ArgHisMetPheValIlePheSerLeuSerTYrIleLeuSerTrpLeu 87
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761 AGATTCAACCTGTTGATCTTGTGCTACACAGTACAGTGGCTTTT 810
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811 CTYTGATATCTGTGCTGATGCTGATACCTGCGGAGATATGACCC 860
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103 . LeuAsnAspProAspIleThrProCysValAspAsnValHisSerPhe 118
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861 ACATAGAGACCCCTCGTGCATCTTGTGTACCAACCTCAGCGGTTT 910
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119 ThrGlyAlaPheLeuPheSerLeuGluThrGlnThrIleGlyTYrGI 135
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911 GTCTGCTCTTTTATTCATCATAGACAGAAACCAACATCGGTATNG 960
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135 YTYrAGCysValThrGluLucySerValAlaValLeuMetValIleL 152
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152 eugInserIleLeuSerCysIleIleAsnThrPheIleIleGlyAlaAla 168
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219 GlnLeuLeuArgTYrThrGluAspSerGluGIYArg...MetThrMetAl 234
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seq_documentation_block:
; Sequence 14, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P
; APPLICANT: Ashford, Michael J
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 14210-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1245 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22..1242
; OTHER INFORMATION: /note= "Encodes a full-length or
; OTHER INFORMATION: nearly full-length human pancreatic beta cell
; OTHER INFORMATION: ATP-sensitive potassium channel protein: Seq ID.
; OTHER INFORMATION: 15."
US-08-385-186-14

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  Quality: 729.50      Length: 331
  Ratio: 2.861        Gaps: 5
  Percent Similarity: 77.039  Percent Identity: 41.994

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54 rGlySerTyrValValAspIlePheThrLeuValAspThrLys 70
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71 ArgHisMetPheValIlePheSerLeuSerTyrIleLeuSerTyrLeu 87
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87 ePheGlySerValPheTyrLeuIleAlaPheHisIleGlyAspLeu... 102
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103 ..LeuAsnAspProAspIleThrProCysValAspAsnValHisSerPhe 118
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seq_documentation_block:
; Sequence 12, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P
; APPLICANT: Ashford, Michael J
; APPLICANT: Bond, Chris T
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1425 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..1330
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; NAME/KEY: misc.feature
; LOCATION: 1..1425
; OTHER INFORMATION: /note="Encodes rat pancreatic beta
; OTHER INFORMATION: cell ATP-sensitive potassium channel protein."
US-08-385-186-12

alignment_scores:
  Quality: 719.50      Length: 331
  Ratio: 2.844        Gaps: 5
  Percent Similarity: 76.435   Percent Identity: 41.994

alignment_block:
US-09-623-304A-1 x US-08-385-186-12 ..
Align seg 1/1 to: US-08-385-186-12 from: 1 to: 1425

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37 uHsLysAspGlySerCysAsnValTyrPheLysHisIlePheGlyGluT 54
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seq_name: /cgn2_6/ptodata/2/ina/5a_COMB.seq:US-08-385-186-1

seq_documentation_block:
; Sequence 1, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P
; APPLICANT: Ashford, Michael J
; TITLE OF INVENTION: BOND, CHRIS T
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 14210-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:

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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385.186
FILING DATE: 07-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/288.510
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/193.372
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..1260
OTHER INFORMATION: /note= "cDNA for rat heart
OTHER INFORMATION: ATP-sensitive potassium channel protein."
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1257
FEATURE:
NAME/KEY: primer_bind
LOCATION: 472..491
OTHER INFORMATION: /note= "Sequence corresponding to
Patent No. 5744594
OTHER INFORMATION: Seq. I.D. No. 5744594 5."
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LOCATION: 632..651
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Patent No. 5744594
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US-08-385-186-3

alignment_scores:
Quality: 714.00 Length: 393
Ratio: 2.644 Gaps: 6
Percent Similarity: 68.702 Percent Identity: 35.878

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Align seg 1/1 to: US-08-385-186-3 from: 1 to: 1260

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7 GGTGATCTAGAGATGCTATGAATCAAGACATGAGATAGACATCACTC 56
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21 oProGluHis..... 24
57 CCAAGACCAACAAGATCCCAACAAGCGCTCGGATTTACATCCCACTTG 106
25 .....IleIleAlaGluLysArgAlaArgArgArg 35

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52 yGluTrpGlySerTyrValValAspIlePheThrThrLeuValAspThr 69
204 GGAACCTACCGCTACCTAGTACCTCTTACACCTGCTGAGACCTCA 253
69 yStrPArgHisMetPheValIlePheSerLeuSerTyrIleLeuSerTrp 85
254 AATGGCGCTTCACCTCTGCTGCTTCAACATGGCTACACCATTTACTGG 303
86 LeuIlePheGlySerValPheTrpLeuIleAlaPheHisHisGlyAspLe 102
304 CTATCTTTGGCTTCATCTGTGCTCATCTTATGTCGAGGTGATCT 353
102 u.....LeuAsnAspProAspIleThrProCysValAspAsnValHis 117
354 GGACCACTGGGTGACCAAGATGCATCCCTGTGTGAATAACCTTAGTG 403
117 erPheThrGlyAlaPheLeuPheSerLeuGluTrpGlnThrThrIleGly 133
404 GCTTGTGTGTCCTTCTCTCTCTTCATTCATGACAGAAACAACATGGG 453
134 TyrGlyTyrArgCysValThrGluGluCysSerValAlaValLeuMetVa 150
454 TATGCTTCAGAGTCATTACAGAAAGTGTCCAGAGGATCATTCCTCT 503
150 IleLeuGlnSerIleLeuSerCysIleIleAsnThrPheIleIleGly 167
504 TCTAGTCAAGCCATCCCTGGCTATTGTTAAAGCTTCATGVTGGGTT 553
167 IaAlaLeuAlaLysMetAlaThrAlaArgLysAspAlaGlnThrIleArg 183
554 GCATGTTTATTAAGATCAGCCAGCAAGAAAGAACAGCAGACCTCATG 603
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854 CTTCTGTGAGATGTCGTGCTCAACTGGAGCAGGAAGATTCGAGGTC 903
279 LeuValThrPheIleTyrThrGlyAspSerThrGlyThrHisGlnSe 295
904 GTGCTACTACTAGAAGGATGTTAGAACCAAGCATGATTCCTCAAGC 953
295 rArgSerSerTyrValProArg**IleLeuTrpGlyHisArgPheAsn 312
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; Sequence 8, Application US/08385186
; Patent No. 5744594
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P
; APPLICANT: Ashford, Michael J
; APPLICANT: Bond, Chris T
; TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM
; TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,186
; FILING DATE: 07-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/288,510
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/193,372
; FILING DATE: 08-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kruse, No. 5744594man J.
; REGISTRATION NUMBER: 35,235
; REFERENCE/DOCKET NUMBER: 14210-2-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1095
; OTHER INFORMATION: /note= "Sequence of cDNA clone
; Patent No. 5744594
; OTHER INFORMATION: encoding a portion of rat pancreatic beta-cell
; OTHER INFORMATION: ATP-sensitive potassium channel protein."
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; NAME/KEY: misc_feature
; LOCATION: 333..366
; OTHER INFORMATION: /note= "Sequence corresponding to
; Patent No. 5744594
; OTHER INFORMATION: Seq. I.D. No. 5744594:7"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1092
US-08-385-186-8

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266 euAspArgIleValAlaIleAspAspAspIleGluIleValThrPhe 282
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698 TCCTCAACCCCGCTGCTTAAGAGAACTGAGATTGTGTCATCCTG 747
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283 IleTyrThrGlyAspSerThrGlyThrSerHisGlnSerArgSerTyr 299
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748 GAGGGAATGGTGGAGCCACGGAATGACGTCGCAAGCTCGAAGCTCTTA 797
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333 GluValTyrAlaProPheCysSerAlaIleGlnLeu 344
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: Sequence 2, Application US/08614155B
: Patent No. 5919692
: GENERAL INFORMATION:
: APPLICANT: Susumu SEINO et al.
: TITLE OF INVENTION: NOVEL UBIQUITOUS POTASSIUM-CHANNEL
: TITLE OF INVENTION: PROTEINS AND THEIR GENES
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
: STREET: 400 Seventh Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/614,155B
: FILING DATE: 12-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 264942/1995
: FILING DATE: 18-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: PLAYER, William E.
: REGISTRATION NUMBER: 31,409
: REFERENCE/DOCKET NUMBER: 10890/P60281USO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-638-6666
: TELEFAX: 202-393-5350
: TELEX: RCA 248593 IDEA UR
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1275 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-614-155B-2

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alignment\_scores: Quality: 698.50 Length: 400  
Ratio: 2.559 Gaps: 7

Percent Similarity: 68.250 Percent Identity: 38.000

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: Patent No. 5670335
: GENERAL INFORMATION:
: APPLICANT: Jan, Lily Y.
: APPLICANT: Jan, Yuh Nung
: APPLICANT: Kubo, Yoshihiro
: APPLICANT: Reuveny, Eitan
: APPLICANT: Slesinger, Paul A.
: TITLE OF INVENTION: Cloning of Mammalian Inward Rectifier
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400

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: CITY: San Francisco
: STATE: California
: COUNTRY: United States
: ZIP: 94111-4187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,690B
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/103,445
: FILING DATE: 06-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Dregier, Walter H.
: REGISTRATION NUMBER: 24,190
: REFERENCE/DOCKET NUMBER: A-58619-1/RHD/JPB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 781-1989
: TELEFAX: (415) 398-3249
: TELEX: 910 277299
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1827 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
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    Ratio: 2.486         Gaps: 7
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alignment_block:
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; Sequence 1, Application US/08486342
; Patent No. 5728535
; GENERAL INFORMATION:
; APPLICANT: Lester, Henry A.
; APPLICANT: Dascal, Nathan
; APPLICANT: Lim, Nancy F.
; APPLICANT: Schreibley, Wolfgang
; APPLICANT: Davidson, No. 5728535man
; TITLE OF INVENTION: DNA Encoding Inward Rectifier,
; TITLE OF INVENTION: G-Protein
; TITLE OF INVENTION: Activated, Mammalian, Potassium KGA Channel and
; TITLE OF INVENTION: Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohnbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,342
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/066,371
; FILING DATE: 21-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,426
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..1534
; US-08-486-342-1

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; Patent No. 5734021
; GENERAL INFORMATION:
; APPLICANT: Lester, Henry A.
; APPLICANT: Dascal, Nathan
; APPLICANT: Lim, Nancy F.
; APPLICANT: Schreimayer, Wolfgang
; APPLICANT: Davidson, No. 5734021man
; TITLE OF INVENTION: DNA Encoding Inward Rectifier,
; TITLE OF INVENTION: G-Protein Activated, Mammalian,
; TITLE OF INVENTION: Potassium KGA Channel and Uses
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr, Hohbach, Test, Albritton
; ADDRESSER: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/473,092
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/066,371
; FILING DATE: 21-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,426
; REFERENCE/DOCKET NUMBER: A-62317/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..1534
; US-08-473-092-1

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    Quality: 696.00      Length: 385
    Ratio: 2.486         Gaps: 7
    Percent Similarity: 72.727    Percent Identity: 36.883

alignment_block:
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103  GCAGGCCAGAGGGGCCAGACAGGGCCACAGCAGCTTGATCCCAANA 152
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seq_documentation_block:
; Sequence 1, Application US/08614801A
; Patent No. 5744524
; GENERAL INFORMATION:
; APPLICANT: Lester, Henry A.
; APPLICANT: Davidson, No. 5744324man
; APPLICANT: Kofuji, Paulo
; TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
; TITLE OF INVENTION: MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Teet, Albrighton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,801A
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/066,371
; FILING DATE: 21-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-63098/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2070 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..1534
; US-08-614-801A-1

alignment_scores:
    Quality: 696.00      Length: 385
    Ratio: 2.486         Gaps: 7
    Percent Similarity: 72.727   Percent Identity: 36.883

alignment_block:
US-09-623-304A-1 x US-08-614-801A-1 ..
Align seg 1/1 to: US-08-614-801A-1 from: 1 to: 2070

4   T Y G I S e r T y r H i s I l e a s n A l a A s p A l a . . . . . 15
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
53  T T T G G G A C A T T A C C A G T A G T A C C A C T T C G T C C A C G G T T C G G G C T T 102
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
16  . . . . . L y s T y r P r o G l y t y r P r o P r o G l u n i s I l e i l a g l u l y s A 30
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
103 G C A G C C C C A G G G G C A G G A C G G G C C C A C A G C A G A C T T G T A C C C A A G A 152
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
30  r g a r g a l a r g a r g a r g l e u H e u H i l y s a s p g l y s e r c y s a s a n l y t y r 46
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
153 A G A A A . . . C G G C A G C G T T C G T G A C A A G A C G T C G T C A T G T C A G 199
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
47  P h e l y H i s I l e p h e g l y l u t r p g l y s e r T y r V a l V a l a s p l i e p h e t h 63
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
200 C A C G C G A C C T G G G C A G C A G A C C A G C A G T C G T T C C A C C T C T T C A C 249
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
63  t r h l e u v a l a s p t h l y s t r p a r g h n s m e t p h e v a l l i e p h e s e r l e u s 80
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
80  e r t y l l e u s e r T r p l e u l i e p h e g l y s e r a l p h e t r p l e u l i e a l a 96
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
300 C C T A C A C C G T G G C C T G C T C T T C A T G C G C T C A T G T G G T G A T G C T 349
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
97  P h e n i s H i s g l y a s p l e u . . . . . l e u a s n a s p r o a s p l i e t h r p r o c y 111
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
350 T A T A C C C G G G G C A C C T G A A C A A G C C A T G T C G G C A A C T A C A C T C C C T G 399
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
111 s v a l a p a n v a l a n i s s e r p h e t h r g l y a l a p h e l e u p h e s e r l e u g l u t 128
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
128 h c g l n t h r t h l i e g l y t y g l y t y r a r g c y s a l t h r g l u g l u c y s s e r 144
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
450 C C G A G G C C A C C A T G G C T A T G G C T A C C G C T A C A T C A C C A A G A T G C C C 499
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
145 V a l l a l e u m e t V a l l e u g l n s e r l i e u s e r c y s i l e i l e a s 161
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
500 G A G G C A T C A T C C T T T C C T T T C A G A T C A T C C T T G C T C A T C G T C G A 549
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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161 n t h r p h e l l e r l e g l y a l a a l e u a l a l y s m e t a l a t h r a l a r g l y s a 178
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
550 C G C T T C C T A T G C G T G C A T G T T C A T C A A G A T G T C C A G C C C A A A A G C 599
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
178 r g a l a g l n t h r l i e a r g p h e s e r T y r p h e a l a l e u l i e g l y m e t a r g a s p 194
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
600 G C G C C A G A C C C T C A T G T T A G C A G C A T G G G G T A T T T C A T G A G G A C 649
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
195 g l y l y s l e u c y s l e u m e t t r p a r g l i e g l y a s p h e a r p r o a s n i s v a 211
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
650 G A A A A C T C A C T C A T G T T C C G G G T G G C A A C C T G C G A C A C C A C A C A T 699
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
211 l v a l g l u g l y t h r v a l a r g a l a g l n l e u l e u a r g t t h r c l u s p s e r g 228
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
700 G C T C C G C G A G A T C C G T G C A A G C T C C A A T C T G G C A G A C A C C T G 749
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
228 l u g l y a r g m e t t h m e t a l a p h e l y s a s p l e u l y s l e u . . . . . 240
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
750 A G G S T G A G T T . . C T A C C C T T G A C C A C T T G A C T G A T G A T G T T 796
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
241 . . . . . V a l a s n a s p g l n l i e l e u v a l t h r p r o v a l t h r l i e a l n i 255
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
797 A G T A C A G G G C A G A T C A A C T T T T C T T G T G T C C C C T C A C A T T T G C A 846
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
255 s g l u l l e a s p h i s g l u s e r p r o l e u t y r a l a l e u a s p a r g l y s a l a v a l a 272
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
847 C G T A T C G A T G C C A A A G C C C T T T T A T G A C T T C C C A G G A A G A C A T G C 896
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
272 l a l y s a s p a n p h e g l u l i e u v a l t h r p h e i l e t y r t h g l y a s p s e r 288
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
897 A A A C T G A A C A G T T C G A G T G T C T C A T C C T G A A G C A T C G T G A A A C C 946
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
289 T h r g l y t h r s e r n i s g l n s e r a r g s e r T y r V a l P r o a r g * * i l e l e 305
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
947 A C A G G A T G A C T T G T C A A G C T G A A C A T C A T A C C A A G A T G A A G T T C T 996
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
305 u t r p g l y n i a r g p h e a s n a s p v a l l e u g l u a l l y s a r g l y s t y r t l 322
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
997 T T G G G G T C A T C G T T T T C C T G T A A T T T C T T T G A A G A A G A T T C T T A 1046
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
322 y s v a l a n c y s l e u g l n p h e g l u g l y s e r a l g u a l t y r a l a p r o p h e 338
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1047 A A G T C A T T A C T C C A G T T C A T G C A A C T T T G A A G T C C C A C C C T C G 1096
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
339 C y s s e r a l a l y s g l n l e u a s p t r p l y s a s p l i n g l n l e u n i s l i e g l y 355
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1097 T A C A G T G T A A A G A G . . . . . C A G G A A G A A T G C T T C T C A T G T C 1134
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355 s a l a p r o p r o v a l a r g l u s e r c y s t h r s e r a s p t h l y s a l a a r g a 372
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1135 T T C C C C T T A A T A G C A C C A G C A T A A C C . . . A A C A G A A A A A A G A C A C A 1181
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
372 r g s e r 373
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1182 A T T C T 1186
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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